

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval  
 Reference Librarian  
 Biotechnology & Chemical Library  
 CM1 1E07 - 703-308-4498  
 jan.delaval@uspto.gov

\*\*\*\*\*  
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Searcher: <u>Jan</u>	Type of Search	Vendors and cost where applicable
Searcher Phone #: <u>4448</u>	NA Sequence (#) _____	STN _____
Searcher Location: _____	AA Sequence (#) <u>✓</u>	Dialog _____
Date Searcher Picked Up: <u>5/27/03</u>	Structure (#) _____	Questel/Orbit _____
Date Completed: <u>5/28/03</u>	Bibliographic _____	Dr. Link _____
Searcher Prep & Review Time: _____	Litigation _____	Lexis/Nexis _____
Clerical Prep Time: <u>10</u>	Fulltext _____	Sequence Systems <u>✓</u>
Online Time: <u>10</u>	Patent Family _____	WWW/Internet _____
	Other _____	Other (specify) _____



Human	flt-3	muteln
Human	flt-3	muteln

Human flt-3 mutein

Human flt-3 mutelin

Canine Flt-3 Ligand

Human Flt-3 ligand

Canine Flt-3 Ligan

Mouse Flt-3 Ligand

Mouse MOT110/T118

FLt3 Ligand FLT10C

Chimeric receptor

Human flt-3 receptor

Flt3L 1-139/IgG2b/

Human flt3 ligand

Trimetric Flt3L-G-C

Human Flt-3 ligand  
Human Flt-3 receptor  
Flt-3 ligand FL14c.  
Human Flt-3 receptor  
Human Flt-3 ligand

FT		/note="extracellular domain may start at position 28"
FT	Domain	183..205
FT		/label=Transmembrane_domain
FT	Domain	206..235
FT		/label=Cytoplasmic_domain
XX		
PN	EP627487-A.	
XX		
XX	07-DEC-1994.	
PD		
XX		
PF	19-MAY-1994;	94EP-0303575.
XX		

PR 24-MAY-1993: 93US-0068394.  
 PR 12-AUG-1993: 93US-0106463.  
 PR 25-AUG-1993: 93US-0111758.  
 PR 03-DEC-1993: 93US-0162407.  
 PR 07-MAR-1994: 94US-0209502.  
 PR 11-MAY-1994: 94US-0243545.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Beckmann MP, Lyman SD;  
 XX  
 DR WPI: 1995-008071/02.  
 DR N-PSDB: AAQ79079.  
 XX  
 PT Isolated ligands for flt 3 receptors - useful for treating  
 PT anemia, AIDS and various cancers  
 XX  
 PS Disclosure: Page 29-30; 33pp; English.  
 XX  
 CC A human T-cell lambda-gt10 random primed cDNA library was  
 CC screened with a fragment corresponding to the extracellular  
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076)  
 CC to isolate human flt3-L cDNA. flt-3 stimulates progenitor and  
 CC stem cells, and can be used e.g. in gene therapy protocols.  
 XX  
 SQ Sequence 235 AA:  
 Query Match 100.0%; Score 1242; DB 16; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVALPAMSPPTYYLLLLLSGSLGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60  
 DB 1 MTVALPAMSPPTYYLLLLLSGSLGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60  
 QY 61 ASNLODEELCGGLMRVLVAQRMERLKTVAAGSKMOGLERVTETIHFYTKCAFOPPSCL 120  
 DB 61 ASNLODEELCGGLMRVLVAQRMERLKTVAAGSKMOGLERVTETIHFYTKCAFOPPSCL 120  
 QY 121 REVQNTISRLQETSEQVALKPWITRONFSKLELQCPDPSSTLPMPSPRPLEATAPT 180  
 DB 121 REVQNTISRLQETSEQVALKPWITRONFSKLELQCPDPSSTLPMPSPRPLEATAPT 180  
 QY 181 APQPLLLLLLLPVGLLLAAAMCLHMORTRRRTRPRGQVPPVSPDILLVEH 235  
 DB 181 APQPLLLLLLLPVGLLLAAAMCLHMORTRRRTRPRGQVPPVSPDILLVEH 235  
 RESULT 2  
 AAM67769 standard; Protein: 235 AA.  
 XX  
 ID AAM67769;  
 XX  
 AC AAM67769;  
 XX  
 DT 25-MAR-1999 (first entry)  
 XX  
 DE Human flt3-ligand.  
 XX  
 KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;  
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;  
 KW tissue transplantation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9857655-A1.  
 XX  
 PD 23-DEC-1998.  
 XX  
 PF 12-JUN-1998: 98WO-US12085.  
 XX  
 PR 17-JUN-1997: 97US-0877421.  
 XX  
 PA (IMMV ) IMMUNEX CORP.

XX  
 PI Abbott NM, Nowat AM, Viney JL;  
 XX  
 DR WPI: 1999-070422/06.  
 DR N-PSDB: AAV81506.  
 XX  
 PT Methods for initiating or enhancing antigen specific immune  
 PT tolerance - by using murine or human flt3 ligand  
 XX  
 PS Claim 1: Page 14-15; 25pp; English.  
 XX  
 CC A method has been developed of initiating or enhancing: (i) an antigen-  
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic  
 CC immunogenic molecule by addition of a polypeptide, before, after or with  
 CC the mucosal administration of an immunotolerizing amount of the antigen  
 CC or therapeutic molecule, respectively. The polypeptide is capable of  
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3  
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino  
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;  
 CC and c) a polypeptide that has at least 90% identity to the polypeptides  
 CC of either (a) or (b). The method ameliorates the effects of autoimmune  
 CC diseases, food allergies or organ or tissue rejection following  
 CC transplantation. Administration of flt3-L allows lower doses of antigens  
 CC to be used in vivo for mucosally administered antigens. The present  
 CC sequence represents human flt3-L.  
 XX  
 SQ Sequence 235 AA:  
 Query Match 100.0%; Score 1242; DB 20; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVALPAMSPPTYYLLLLLSGSLGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60  
 DB 1 MTVALPAMSPPTYYLLLLLSGSLGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60  
 QY 61 ASNLODEELCGGLMRVLVAQRMERLKTVAAGSKMOGLERVTETIHFYTKCAFOPPSCL 120  
 DB 61 ASNLODEELCGGLMRVLVAQRMERLKTVAAGSKMOGLERVTETIHFYTKCAFOPPSCL 120  
 QY 121 REVQNTISRLQETSEQVALKPWITRONFSKLELQCPDPSSTLPMPSPRPLEATAPT 180  
 DB 121 REVQNTISRLQETSEQVALKPWITRONFSKLELQCPDPSSTLPMPSPRPLEATAPT 180  
 QY 181 APQPLLLLLLLPVGLLLAAAMCLHMORTRRRTRPRGQVPPVSPDILLVEH 235  
 DB 181 APQPLLLLLLLPVGLLLAAAMCLHMORTRRRTRPRGQVPPVSPDILLVEH 235  
 RESULT 3  
 AAY69719 standard; Protein: 235 AA.  
 XX  
 ID AAY69719;  
 XX  
 AC AAY69719;  
 XX  
 DT 05-JUL-2000 (first entry)  
 XX  
 DE Full length wild type human flt-3 protein.  
 XX  
 KW Immunomodulator; immunosuppressive; cytostatic; antineoplastic; anti-HIV;  
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 KW cellular expansion; cellular differentiation; natural killer cell;  
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 KW multiple myeloma; leukemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200001823-A2.  
 XX  
 PD 13-JAN-2000.  
 XX

PF 25-JUN-1999; 99WO-US14296.  
 XX 02-JUL-1998; 98US-0109100.  
 XX (IMMUNEX CORP.  
 PA Graddis TJ, McGrew JT;  
 PI WPI: 2000-182115/16.  
 DR N-PSDB; AA259064.  
 XX  
 XX  
 PS Claim 1: Page 72-73; 90pp; English.  
 PT The invention relates to novel soluble flt-3 ligand (flt-3-L) polypeptides  
 PT which exhibits increased or decreased biological activity relative to  
 CC the full length wild type (this sequence) or mature (AA69720) flt-3-L  
 CC polypeptides. The flt-3-L protein binds cell surface tyrosine kinase  
 CC receptors and regulate growth and differentiation of hematopoietic  
 CC progenitor cells. The flt-3-L protein can be used to induce cellular  
 CC expansion (especially in vivo) or differentiation, e.g. in  
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the  
 CC presence of growth factors such as interleukins, colony stimulating  
 CC factors or protein kinases. The protein can also modulate, augment or  
 CC enhance a patient's immune response and can be used to treat an immune  
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein  
 CC may be used to treat a pathological condition e.g. myelodysplasia,  
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or  
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute  
 CC leukemia.  
 CC  
 SQ Sequence 235 AA;  
 Query Match 100.0%; Score 1242; DB 21; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVLAPAMSPPTTYLLLLLSGLSGTGPCSFQHSPTSSDFAVKIRELSYLDYDPVTV 60  
 DB 1 MTVLAPAMSPPTTYLLLLLSGLSGTGPCSFQHSPTSSDFAVKIRELSYLDYDPVTV 60  
 QY 61 ASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMGLLEVRNTEHFVTKCAFPSPSC 120  
 DB 61 ASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMGLLEVRNTEHFVTKCAFPSPSC 120  
 QY 121 RRVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCPDSSSTLPSPRLEATAPT 180  
 DB 121 RRVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCPDSSSTLPSPRLEATAPT 180  
 QY 181 AROPPLLLLLLPGVLLLAAMCLHMORTRRTPRGQVPPVPSPOLLVENH 235  
 DB 181 AROPPLLLLLLPGVLLLAAMCLHMORTRRTPRGQVPPVPSPOLLVENH 235  
 RESULT 4  
 AAB20192  
 ID AAB20192 standard; Protein: 235 AA.  
 XX AAB20192;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Human flt-3 ligand.  
 XX  
 KW Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;  
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;  
 KW lymphoma; autoimmune disease; infection; gene therapy  
 XX  
 OS Homo sapiens.  
 XX

FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /label= signal\_peptide  
 FT Protein 27..235  
 FT /label= Mature-protein  
 FT Domain 27..182  
 FT /label= Extracellular\_domain  
 FT Domain 183..205  
 FT /label= Transmembrane\_domain  
 FT Domain 206..235  
 FT /label= Cytoplasmic\_domain  
 PN WO200109303-A2.  
 PD 08-FEB-2001.  
 PR 31-JUL-2000; 2000WO-US20679.  
 PR 30-JUL-1999; 99US-0146170.  
 PA (VICA-) VICAL INC.  
 PI Hermanson GG;  
 DR WPI: 2001-123319/13.  
 DR N-PSDB; AAF30310.  
 PT Immunogenic compositions comprising flt-3 ligand encoding  
 PT polynucleotide and one or more antigen, or cytokine encoding  
 PT polynucleotides, useful for suppressing tumour growth and for treating  
 PT autoimmune diseases (e.g. rheumatoid arthritis) -  
 XX  
 PS Claim 2: Page 132-133; 149pp; English.  
 XX  
 CC The present sequence is that of human Fms-like tyrosine kinase  
 CC (flt-3 ligand). The invention is directed to enhancing the  
 CC immune response of a vertebrate to an antigen or a cytokine by  
 CC administering in vivo, into a tissue of a vertebrate, a flt-3  
 CC ligand-encoding polynucleotide, and 1 or more antigen- or  
 CC cytokine-encoding polynucleotides. The flt-3 ligand-encoding  
 CC polynucleotide may encode the present full-length human flt-3  
 CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,  
 CC or 27-235 of the ligand. The polynucleotides are incorporated  
 CC into the cells of the vertebrate in vivo, and a prophylactically  
 CC or therapeutically effective amount of flt-3 ligand and 1 or more  
 CC antigens or cytokines is produced in vivo. Pharmaceutical  
 CC compositions comprising the polynucleotides are useful for  
 CC suppressing tumour growth in a mammal. The tumour is melanoma,  
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also  
 CC be used for the prophylactic and/or therapeutic treatment of:  
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B  
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;  
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and  
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
 CC Various other examples of these diseases are given in the  
 CC specification.  
 CC  
 SQ Sequence 235 AA;  
 Query Match 100.0%; Score 1242; DB 22; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVLAPAMSPPTTYLLLLLSGLSGTGPCSFQHSPTSSDFAVKIRELSYLDYDPVTV 60  
 DB 1 MTVLAPAMSPPTTYLLLLLSGLSGTGPCSFQHSPTSSDFAVKIRELSYLDYDPVTV 60  
 QY 61 ASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMGLLEVRNTEHFVTKCAFPSPSC 120  
 DB 61 ASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMGLLEVRNTEHFVTKCAFPSPSC 120  
 QY 121 RRVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCPDSSSTLPSPRLEATAPT 180  
 DB 121 RRVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCPDSSSTLPSPRLEATAPT 180

Db 121 RFVOTNISRLQETSEQLVAKPWITRONFSKCLEQCPDSSSTLPMPSPRLTAAPT 180

QY 181 APQPLLILLLLPVGLLLLAAMCLHMOTRRRTTRPRGQVPPVPSPODLLVEH 235  
 |||||

Db 181 APQPLLILLLLPVGLLLLAAMCLHMOTRRRTTRPRGQVPPVPSPODLLVEH 235  
 |||||

RESULT 5  
 ABB08129  
 ID ABB08129 standard; protein: 235 AA.  
 XX  
 AC ABB08129;  
 XX  
 DT 10-SEP-2002 (first entry)  
 XX  
 DE Human Flt3L polypeptide.  
 XX  
 KM Dendritic cell: mobilisation factor: T cell; adjuvant: antibacterial;  
 KM fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;  
 KM tuberculostatic; cytosstatic; human; Flt3L.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200236141-A2.  
 XX  
 PD 10-MAY-2002.  
 XX  
 PF 30-OCT-2001; 2001WO-US44834.  
 XX  
 PR 02-NOV-2000; 2000US-245721P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE  
 PI Thomas EK;  
 XX  
 DR WPI: 2002-500114/53.  
 XX  
 PT Treating an individual suffering from infection, e.g. inflammation,  
 PT chickenpox or AIDS, by administering a combination of dendritic cell  
 PT mobilization factor or maturation agent, T cell enhancing factor and  
 PT antigen-specific T cells -  
 XX  
 PS Disclosure: Page 37-38; 43pp; English.

CC The invention relates to treating an individual at risk for or suffering  
 CC from infection with a pathogenic or opportunistic organism. The method  
 CC involves administering a combination of two to five agents comprising:  
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation  
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;  
 CC or (e) activated, antigen specific T cells. The methods are useful for  
 CC treating an individual at risk for or suffering from infection with a  
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria  
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.  
 CC T. cruzi, which causes Chagas's disease). The methods are especially  
 CC useful for treating an individual suffering from immunosuppression by  
 CC enhancing a lymphocyte-mediated immune response. In particular, the  
 CC method is useful for treating inflammations, chickenpox, oral or genital  
 CC herpes, mononucleosis, multilocal leukoencephalopathy, hepatitis, AIDS,  
 CC T cell leukemia or T cell lymphoma. The activated antigen-presenting  
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence  
 CC represents a human Flt3L polypeptide fragment, that can be used as a  
 CC dendritic cell mobilisation factor.

XX  
 S0 Sequence 235 AA:  
 Query Match 100.0%; Score 1242; DB 23; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPANSPPTVYLLLLLSGSLGTDGCFQHSPISSDPAVKIRELSDVLEADYPTV 60  
 |||||  
 Db 1 MTVLAPANSPPTVYLLLLLSGSLGTDGCFQHSPISSDPAVKIRELSDVLEADYPTV 60  
 |||||

QY 61 ASNLODEELGGLMRLVLAQRMERLKTIVAGSKMOLLERVTETHEFVTKCAFOPPPSCL 120  
 |||||

Db 61 ASNLODEELGGLMRLVLAQRMERLKTIVAGSKMOLLERVTETHEFVTKCAFOPPPSCL 120  
 |||||

QY 121 RFVOTNISRLQETSEQLVAKPWITRONFSKCLEQCPDSSSTLPMPSPRLTAAPT 180  
 |||||

Db 121 RFVOTNISRLQETSEQLVAKPWITRONFSKCLEQCPDSSSTLPMPSPRLTAAPT 180  
 |||||

QY 181 APQPLLILLLLPVGLLLLAAMCLHMOTRRRTTRPRGQVPPVPSPODLLVEH 235  
 |||||

Db 181 APQPLLILLLLPVGLLLLAAMCLHMOTRRRTTRPRGQVPPVPSPODLLVEH 235  
 |||||

RESULT 6  
 AAR66175  
 ID AAR66175 standard; peptide: 235 AA.  
 XX  
 AC AAR66175;  
 XX  
 DT 10-AUG-1995 (first entry)  
 XX  
 DE Human S86/S109 Flt3 ligand peptide sequence.  
 XX  
 KM Flt3 ligand; tyrosine kinase receptor ligand.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9426891-A.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 18-MAY-1994; 94WO-US05150.  
 XX  
 PR 19-MAY-1993; 93US-0065231.  
 PR 07-JUL-1993; 93US-0089263.  
 PR 16-JUL-1993; 93US-0092549.  
 PR 13-AUG-1993; 93US-0106340.  
 PR 24-AUG-1993; 93US-0112391.  
 PR 19-NOV-1993; 93US-0155111.  
 PR 03-DEC-1993; 93US-0162413.  
 XX  
 PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Birnbaum D, Cuipepper JA, Hannum CH, Lee FD;  
 XX  
 DR WPI: 1995-006787/01.  
 XX  
 N-PSDB; AAQ79642.

PT New ligand for the Flt3 tyrosine kinase receptor - and related  
 PT nucleic acid, vectors, host cells and antibodies, useful for  
 PT treating abnormal cell physiology and proliferation, e.g. cancer,  
 PT also for diagnosis and drug screening  
 XX  
 PS Claim 11; Page 76-77; 90pp; English.

CC A cDNA library from the human stromal cell line 293SV48, in  
 CC pMT185, was screened with an 800 bp fragment derived from  
 CC mouse clone T118. This fragment encompasses the coding region  
 CC conserved between two mouse clones, T118 and T110. Approx. 20  
 CC positive clones were selected and partially sequenced. Two  
 CC clones, S86 and S109, were found to be approx. 75% homologous  
 CC to the mouse clones over the first 163 AAs. Clone S86 continued  
 CC to show homology to T110 until the stop codon, although to a  
 CC lesser degree, for an overall homology of 66%. Clones T118 and  
 CC S109 do not show homology to each other or to the other clones  
 CC after mouse residue 163 (human residue 160). An additional mouse  
 CC clone designated M88 has a 29 AA insert at the junction between  
 CC the common and divergent portions of the mouse ligand.

XX  
 S0 Sequence 235 AA:

Query Match 99.5%; Score 1236; DB 16; Length 235;  
 Best Local Similarity 99.6%; Pred. No. 1.8e-108;  
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPPTTYLLLLLLSSGSGTQDCSFQHSPISSDPVAVKIRELSIDLDDYPTV 60  
 D 1 MTVLAPAWSPPTTYLLLLLLSSGSGTQDCSFQHSPISSDPVAVKIRELSIDLDDYPTV 60  
 QY 61 ASNLODELGCGLMRLVLAQRMERLKTVAASKMOGLLEVRNTEIHFTKCAFQPPSCL 120  
 D 61 ASNLODELGCGLMRLVLAQRMERLKTVAASKMOGLLEVRNTEIHFTKCAFQPPSCL 120  
 QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELOCQCPDSSSTLPPWSPRPLEATAPT 180  
 D 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELOCQCPDSSSTLPPWSPRPLEATAPT 180  
 QY 181 APQPPULLLLLPVGLLLLAAMCLHMORTRRRPRPEGVPPVPSPDOLLVEH 235  
 D 181 APQPPULLLLLPVGLLLLAAMCLHMORTRRRPRPEGVPPVPSPDOLLVEH 235

RESULT 7  
 AAB20194  
 ID AAB20194 standard; Protein: 235 AA.  
 AC AAB20194;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Human Flt-3 ligand.  
 XX  
 KW Flt-3 ligand; fms-like tyrosine kinase; human; vaccine;  
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;  
 KW lymphoma; autoimmune disease; infection; gene therapy.  
 XX  
 OS Homo sapiens.  
 FH  
 FT Key Location/Qualifiers  
 FT Peptide 1..26  
 FT Protein /label= Signal\_peptide  
 FT 27..235  
 FT /label= Mature\_protein  
 FT Domain 27..182  
 FT /label= Extracellular\_domain  
 FT Domain 183..205  
 FT /label= Transmembrane\_domain  
 FT Domain 206..235  
 FT /label= Cytoplasmic\_domain  
 FT  
 XX  
 PN WO200109303-A2.  
 PN  
 PD 08-FEB-2001.  
 PD  
 PE 31-JUL-2000; 2000WO-US20679.  
 PE  
 PR 30-JUL-1999; 99US-0146170.  
 PR  
 PA (VICA-) VICAL INC.  
 PA  
 PI Hermanson GG;  
 PI  
 XX N-PSDB; AAF30312.  
 DR  
 DR  
 DR  
 PT Immunogenic compositions comprising Flt-3 ligand encoding  
 PT polynucleotide and one or more antigen, or cytokine encoding  
 PT polynucleotides, useful for suppressing tumour growth and for treating  
 PT autoimmune diseases (e.g. rheumatoid arthritis)  
 XX  
 PS Claim 2; Page 137-138; 149pp; English.  
 PS  
 CC The present sequence is that of human fms-like tyrosine kinase  
 CC (flt-3 ligand). The invention is directed to enhancing the

CC immune response of a vertebrate to an antigen or a cytokine by  
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3  
 CC ligand-encoding polynucleotide, and 1 or more antigen- or  
 CC cytokine-encoding polynucleotides. The flt-3 ligand-encoding  
 CC polynucleotide may encode the present full-length human flt-3  
 CC ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235  
 CC of the flt-3 ligand. The polynucleotides are incorporated into  
 CC the cells of the vertebrate in vivo, and a prophylactically or  
 CC therapeutically effective amount of flt-3 ligand and 1 or more  
 CC antigens or cytokines is produced in vivo. Pharmaceutical  
 CC compositions comprising the polynucleotides are useful for  
 CC suppressing tumour growth in a mammal. The tumour is melanoma,  
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also  
 CC be used for the prophylactic and/or therapeutic treatment of:  
 CC (a) bacterial (e.g. bacillus infections), viral (e.g. hepatitis B  
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;  
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and  
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
 CC Various other examples of these diseases are given in the  
 CC specification.

Sequence 235 AA;  
 SQ

Query Match 99.5%; Score 1236; DB 22; Length 235;  
 Best Local Similarity 99.6%; Pred. No. 1.8e-108;  
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPPTTYLLLLLLSSGSGTQDCSFQHSPISSDPVAVKIRELSIDLDDYPTV 60  
 D 1 MTVLAPAWSPPTTYLLLLLLSSGSGTQDCSFQHSPISSDPVAVKIRELSIDLDDYPTV 60  
 QY 61 ASNLODELGCGLMRLVLAQRMERLKTVAASKMOGLLEVRNTEIHFTKCAFQPPSCL 120  
 D 61 ASNLODELGCGLMRLVLAQRMERLKTVAASKMOGLLEVRNTEIHFTKCAFQPPSCL 120  
 QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELOCQCPDSSSTLPPWSPRPLEATAPT 180  
 D 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELOCQCPDSSSTLPPWSPRPLEATAPT 180  
 QY 181 APQPPULLLLLPVGLLLLAAMCLHMORTRRRPRPEGVPPVPSPDOLLVEH 235  
 D 181 APQPPULLLLLPVGLLLLAAMCLHMORTRRRPRPEGVPPVPSPDOLLVEH 235

RESULT 8  
 AAY69721  
 ID AAY69721 standard; Protein: 212 AA.  
 AC AAY69721;  
 XX  
 DT 05-JUL-2000 (first entry)  
 DT  
 DE Human flt-3 mutein L-3H.  
 DE  
 XX  
 KW Immunomodulator; immunosuppressive; cytostatic; anti-leukemia; anti-HIV;  
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 KW cellular expansion; cellular differentiation; natural killer cell;  
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 KW multiple myeloma; leukemia; mutein.  
 XX  
 OS Homo sapiens.  
 OS  
 OS Synthetic.  
 PN WO200001823-A2.  
 PN  
 PD 13-JAN-2000.  
 PD  
 PE 25-JUN-1999; 99WO-US41296.  
 PE  
 PR 02-JUL-1998; 98US-0109100.  
 PR  
 XX

XX	07-MAY-1998.
FF	23-OCT-1997; 97MO-US18700.
XX	
PR	25-OCT-1996; 96US-0030094.
XX	
PA	(SEAR ) SEARLE & CO G D.
XX	
P1	Feng Y, McKearn JP, McWhorter CA, Minerly JC, Minster NI;
PI	Staten NR, Streeter PR, Wolfe SL;
XX	
DR	WI; 1998-272218/24.
PS	
XX	Disclosure; Page 9-10; 158pp; English.
CC	
CC	This sequence represents a rearranged human flt-3 receptor agonists of
CC	the invention. The agonists have a modified flt-3 ligand amino acid
CC	sequence. The agonists are used to stimulate production of haematopoietic
CC	cells in vivo (e.g. in a subject about to donate blood) or for ex vivo
CC	expansion for subsequent transplantation, e.g. to reconstitute bone
CC	marrow after chemotherapy, disease etc., or to treat haematological
CC	diseases such as drug-induced myelosuppression, defects caused by
CC	infections, burns or renal dialysis. Optionally ex vivo expanded cells
CC	are transduced with a gene therapy vector for treating e.g. congenital
CC	metabolic diseases, immune deficiency, neurological disease, cancer and
CC	infections. The agonists can also be used in the treatment of tumours,
CC	infections and autoimmune disease, when administered optionally with an
CC	antigen. The agonist can also be used in the production of dendritic
CC	cells for use as an immunising adjuvant for treatment disorders including
CC	acquired immune deficiency syndrome. Compared with native ligands, the
CC	new agonists have better stimulatory activity, reduced side effects
CC	and/or better physical properties such as solubility, stability or refold
CC	efficiency. When used together with other stimulatory agents, the
CC	agonists provide a synergistic effect.
XX	
XX	
SQ	Sequence 209 AA:
	Query Match 89.7%; Score 114; DB 19; Length 209;
	Best Local Similarity 100.0%; Pred. No. 5.1e-97;
	Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	27 TQDCSFQHSPISSDFAVKIRELSIDLDDYVTVASNLQDELGGIMRLVLAQRMRRL 86
Db	1 TDQCSFQHSPISSDFAVKIRELSIDLDYDVTVASNLQDELGGLMRLVLAQRMRRL 60
OY	87 KTVAGSKQGGLERNTNFIHVTKCAFPSPSCRFVOTNSRILQETSSEQLVALKPMT 146
Db	61 KTVAGSKQGGLERNTNFIHFVTKCAFPPSPCLFEVOTNSRILQETSEQLVALKPMT 120
OY	147 RQNSRCLELCCOPDSSITLPWWSBRPLEATAPAPOPPLLLLLLLPYGILLAAACLIH 206
Db	121 RQNSRCLELCCQPDSSITLPWPWSBRPLEATAPAPAPPLLLLLLLPYGLLLAAACLIH 180
OY	207 WQTRRRRTPRPEGVPPVPSPQDLLVEH 235
Db	181 WQTRRRRTPRPEGVPPVPSPQDLLVEH 209
RESULT 10	
ID	AAI69720
TT	AAV69720 standard; Protein: 209 AA.
XX	
AC	AAV69720;
XX	
DT	05-JUL-2000 (first entry)
DE	Mature wild type human flt-3 protein.
XX	





Db 121 RQNFSCLELQCPDSSSTLPSPSPRELEATAPAPQPLLILLPLVGLLLAAACLH 180  
 QY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235  
 Db 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209

## RESULT 12

AAV69726 standard; Protein: 209 AA.

AAV69726;

05-JUL-2000 (first entry)

Human flt-3 mutein Q122R.

Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;  
 neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;  
 cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 cellular expansion; cellular differentiation; natural killer cell;  
 cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 multiple myeloma; leukemia; mutein.

Homo sapiens.  
 Synthetic.

MO200001823-A2.

13-JAN-2000.

25-JUN-1999; 99WO-US14296.

02-JUL-1998; 98US-0109100.

(IMMV ) IMMUNEX CORP.

Graddis TJ, McGrew JT;

WPI; 2000-182115/16.

Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
 immune response stimulation or treatment of pathological conditions  
 PT contains amino acid substitutions at positions 8, 84, 118 or 122  
 XX  
 PS Claim 4; Page 88-89; 90pp; English.

The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
 CC which exhibits increased or decreased biological activity relative to  
 CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L  
 CC polypeptides. This sequence represents an example of the novel flt-3  
 CC ligands and comprises the Q122R mutant polypeptide. The flt3-L protein  
 CC binds cell surface tyrosine kinase receptors and regulate growth and  
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
 CC be used to induce cellular expansion (especially in vivo) or  
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
 CC cells, especially in the presence of growth factors such as interleukins,  
 CC colony stimulating factors or protein kinases. The protein can also  
 CC modulate, augment or enhance a patient's immune response and can be used  
 CC to treat an immune disorder (e.g. allergy, autoimmunity or  
 CC immunosuppression). The protein may be used to treat a pathological  
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
 CC myeloma, neuroblastoma or acute leukemia.

Sequence 209 AA;

Query Match

Best Local Similarity 89.4%; Score 1110; DB 21; Length 209;  
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDQSFQHSPISSDFAVKIRELSDYLLQDYPVTVAASNLODELCGGLMRLVLAQRMMERL 86

Db 1 TDQSFQHSPISSDFAVKIRELSDYLLQDYPVTVAASNLODELCGGLMRLVLAQRMMERL 60  
 QY 87 KTVAGSKMOGLLEAVNEIHFVTKCAFQPPSCIRFQTNISRLQETSEDLVAKPMIT 146  
 Db 61 KTVAGSKMOGLLEAVNEIHFVTKCAFQPPSCIRFQTNISRLQETSEDLVAKPMIT 120  
 QY 147 RQNFSCLELQCPDSSSTLPSPSPRELEATAPAPQPLLILLPLVGLLLAAACLH 206  
 Db 121 RQNFSCLELQCPDSSSTLPSPSPRELEATAPAPQPLLILLPLVGLLLAAACLH 180

## RESULT 13

AAV69727 standard; Protein: 209 AA.

AAV69727;

05-JUL-2000 (first entry)

Human flt-3 mutein L26F.

Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;  
 neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;  
 cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 cellular expansion; cellular differentiation; natural killer cell;  
 cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 multiple myeloma; leukemia; mutein.

Homo sapiens.  
 Synthetic.

MO200001823-A2.

13-JAN-2000.

25-JUN-1999; 99WO-US14296.

02-JUL-1998; 98US-0109100.

(IMMV ) IMMUNEX CORP.

Graddis TJ, McGrew JT;

WPI; 2000-182115/16.

Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
 immune response stimulation or treatment of pathological conditions  
 PT contains amino acid substitutions at positions 8, 84, 118 or 122  
 XX  
 PS Claim 13; Page 82-83; 90pp; English.

The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
 CC which exhibits increased or decreased biological activity relative to  
 CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L  
 CC polypeptides. This sequence represents an example of the novel flt-3  
 CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein  
 CC binds cell surface tyrosine kinase receptors and regulate growth and  
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
 CC be used to induce cellular expansion (especially in vivo) or  
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
 CC cells, especially in the presence of growth factors such as interleukins,  
 CC colony stimulating factors or protein kinases. The protein can also  
 CC modulate, augment or enhance a patient's immune response and can be used  
 CC to treat an immune disorder (e.g. allergy, autoimmunity or  
 CC immunosuppression). The protein may be used to treat a pathological  
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple

CC myeloma, neuroblastoma or acute leukemia.  
XX Sequence 209 AA;  
SQ  
Query Match 89.4%; Score 1110; DB 21; Length 209;  
Best Local Similarity 99.5%; Pred. No. 1.2e-96;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 27 TODCSFQHSPISSDFAVKIRELSIDYLLQDYPVTASNLQDEELCGGLMRLVLAQRMWERL 86  
DB 1 TODCSFQHSPISSDFAVKIRELSIDYLLQDYPVTASNLQDEELCGGLMRLVLAQRMWERL 60  
OY 87 KTVAGSKMOGLLERYNTEHFVTKCAFPSPCLRFVOTNISRLQETSEQLVALKPWIT 146  
DB 61 KTVAGSKMOGLLERYNTEHFVTKCAFPSPCLRFVOTNISRLQETSEQLVALKPWIT 120  
OY 147 RQNSRCLELQCCPDSSSTLPPWSPRPLEATPTAPQPLLILLPVGILLAAACWCH 206  
DB 121 RQNSRCLELQCCPDSSSTLPPWSPRPLEATPTAPQPLLILLPVGILLAAACWCH 180  
OY 207 WQTRRRRTPRGEGVPPVPSQDILLVEH 235  
DB 181 WQTRRRRTPRGEGVPPVPSQDILLVEH 209  
RESULT 14  
AAV69729 standard; Protein: 209 AA.  
XX  
AC AAV69729;  
XX 05-JUL-2000 (first entry)  
XX Human flt-3 mutleln A64T.  
XX  
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;  
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
KW cellular expansion; cellular differentiation; natural killer cell;  
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
KW multiple myeloma; leukemia; mutleln.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001823-A2.  
XX  
PD 13-JAN-2000.  
XX  
PF 25-JUN-1999; 99WO-US14296.  
XX  
PR 02-JUL-1998; 98US-0109100.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Graddis TJ, McGrew JT;  
XX  
DR WPI: 2000-182115/16.  
XX  
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
PT immune response stimulation or treatment of pathological conditions  
PT contains amino acid substitutions at positions 8, 84, 118 or 122  
XX  
PS Claim 13; Page 78-79; 90pp; English.  
XX  
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
CC which exhibits increased or decreased biological activity relative to  
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L.  
CC polypeptides. This sequence represents an example of the novel flt3  
CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein  
CC binds cell surface tyrosine kinase receptors and regulate growth and  
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can

CC be used to induce cellular expansion (especially in vivo) or  
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
CC cells, especially in the presence of growth factors such as interleukins,  
CC colony stimulating factors or protein kinases. The protein can also  
CC modulate, augment or enhance a patient's immune response and can be used  
CC to treat an immune disorder (e.g. allergy, autoimmunity or  
CC immunosuppression). The protein may be used to treat a pathological  
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
CC myeloma, neuroblastoma or acute leukemia.  
XX  
SQ Sequence 209 AA;  
Query Match 89.4%; Score 1110; DB 21; Length 209;  
Best Local Similarity 99.5%; Pred. No. 1.2e-96;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 27 TODCSFQHSPISSDFAVKIRELSIDYLLQDYPVTASNLQDEELCGGLMRLVLAQRMWERL 86  
DB 1 TODCSFQHSPISSDFAVKIRELSIDYLLQDYPVTASNLQDEELCGGLMRLVLAQRMWERL 60  
OY 87 KTVAGSKMOGLLERYNTEHFVTKCAFPSPCLRFVOTNISRLQETSEQLVALKPWIT 146  
DB 61 KTVAGSKMOGLLERYNTEHFVTKCAFPSPCLRFVOTNISRLQETSEQLVALKPWIT 120  
OY 147 RQNSRCLELQCCPDSSSTLPPWSPRPLEATPTAPQPLLILLPVGILLAAACWCH 206  
DB 121 RQNSRCLELQCCPDSSSTLPPWSPRPLEATPTAPQPLLILLPVGILLAAACWCH 180  
OY 207 WQTRRRRTPRGEGVPPVPSQDILLVEH 235  
DB 181 WQTRRRRTPRGEGVPPVPSQDILLVEH 209  
RESULT 15  
AAV69722 standard; Protein: 209 AA.  
XX  
AC AAV69722;  
XX  
DT 05-JUL-2000 (first entry)  
XX  
XX Human flt-3 mutleln H8Y.  
XX  
DE  
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;  
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
KW cellular expansion; cellular differentiation; natural killer cell;  
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
KW multiple myeloma; leukemia; mutleln.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200001823-A2.  
XX  
PD 13-JAN-2000.  
XX  
PF 25-JUN-1999; 99WO-US14296.  
XX  
PR 02-JUL-1998; 98US-0109100.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Graddis TJ, McGrew JT;  
XX  
DR WPI: 2000-182115/16.  
XX  
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
PT immune response stimulation or treatment of pathological conditions  
PT contains amino acid substitutions at positions 8, 84, 118 or 122  
XX

PS Claim 4; Page 81-82; 90pp; English.

XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
 CC which exhibit increased or decreased biological activity relative to  
 CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L  
 CC polypeptides. This sequence represents an example of the novel flt-3  
 CC ligands and comprises the H81 mutant polypeptide. The flt3-L protein  
 CC binds cell surface tyrosine kinase receptors and regulate growth and  
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
 CC be used to induce cellular expansion (especially in vivo) or  
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
 CC cells, especially in the presence of growth factors such as interleukins,  
 CC colony stimulating factors or protein kinases. The protein can also  
 CC modulate, augment or enhance a patient's immune response and can be used  
 CC to treat an immune disorder (e.g. allergy, autoimmunity or  
 CC immunosuppression). The protein may be used to treat a pathological  
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
 CC myeloma, neuroblastoma or acute leukemia.

XX Sequence 209 AA;

Query Match 89.2%; Score 1108; DB 21; Length 209;  
 Best Local Similarity 99.5%; Pred. No. 1.9e-96;  
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDPAVKIRELSDYLLQDYPPVVASNLQDELCGLMRLVLAQRWHERL 86  
 DB 1 TODCSFQHSPISSDPAVKIRELSDYLLQDYPPVVASNLQDELCGLMRLVLAQRWHERL 60  
 QY 87 KYVAGSKMOGLLEVRNTEIHVTKCAFOPPSCIREYQINISRLQETSEQLVALKEWIT 146  
 DB 61 KYVAGSKMOGLLEVRNTEIHVTKCAFOPPSCIREYQINISRLQETSEQLVALKEWIT 120  
 QY 147 RQNFSCLELEQCCPDSSSTLPPWSPRLDEATAPOPLLLLELPVGLLAAAMCCH 206  
 DB 121 RQNFSCLELEQCCPDSSSTLPPWSPRLDEATAPOPLLLLELPVGLLAAAMCCH 180  
 QY 207 WQTRRRTPRRGEQVPPVPSPODLLVEH 235  
 DB 181 WQTRRRTPRRGEQVPPVPSPODLLVEH 209

Search completed: May 27, 2003, 18:27:13  
 Job time : 37 secs

GenCore version 5.1.4-p5.4578  
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## OM protein - protein search, using sw model

Run on: May 27, 2003, 18:26:36 : Search time 15 Seconds  
(without alignments)  
460.959 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242

Sequence: 1 MVLAPAWSPFTYLLLL...RPGGVPPVPSQDLLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfilltest.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1	US-08-243-545-6
2	1242	100.0	235	2	US-08-993-962-6
3	1242	100.0	235	4	US-09-150-841-6
4	1242	100.0	235	4	US-09-109-100-1
5	1242	100.0	235	5	PCT-US94-05365-6
6	1124	90.5	212	4	US-09-109-100-10
7	1114	89.7	209	4	US-09-109-100-18
8	1110	89.4	209	4	US-09-109-100-9
9	1110	89.4	209	4	US-09-109-100-12
10	1110	89.4	209	4	US-09-109-100-14
11	1110	89.4	209	4	US-09-109-100-17
12	1108	89.2	209	4	US-09-109-100-11
13	1108	89.2	209	4	US-09-109-100-15
14	1107	89.1	209	4	US-09-109-100-13
15	1106	89.0	209	4	US-09-109-100-8
16	1100	88.6	209	4	US-09-109-100-15
17	768.5	61.9	231	1	US-08-243-545-2
18	768.5	61.9	231	2	US-08-993-962-2
19	768.5	61.9	231	4	US-09-160-841-2
20	768.5	61.9	231	5	PCT-US94-05365-2
21	765.5	61.6	231	1	US-08-220-3798-7
22	765.5	61.6	231	5	PCT-US95-03866-6
23	506.5	40.8	137	4	US-09-109-100-15
24	154	12.4	42	5	PCT-US94-05150-17
25	91.5	7.4	675	1	US-08-317-522A-5
26	91.5	7.4	675	1	US-08-439-818A-9
27	91.5	7.4	675	2	US-08-751-965-9

28	91.5	7.4	675	2	US-08-738-975-9	Sequence 9, Appl1
29	91.5	7.4	675	2	US-08-728-626-9	Sequence 9, Appl1
30	91.5	7.4	675	2	US-08-808-559A-9	Sequence 9, Appl1
31	87.5	7.0	415	4	US-09-006-353A-6	Sequence 6, Appl1
32	87.5	7.0	415	4	US-09-573-986-6	Sequence 6, Appl1
33	85	6.8	366	1	US-08-004-492-8	Sequence 8, Appl1
34	84.5	6.8	913	3	US-08-445-640-4	Sequence 4, Appl1
35	84.5	6.8	913	3	US-08-170-558-4	Sequence 4, Appl1
36	84.5	6.8	913	3	US-08-447-314-4	Sequence 4, Appl1
37	84.5	6.8	913	3	US-08-445-451-4	Sequence 4, Appl1
38	84	6.8	107	4	US-09-220-528-52	Sequence 52, Appl1
39	84	6.8	220	4	US-09-220-528-26	Sequence 26, Appl1
40	83.5	6.7	429	1	US-07-964-589-2	Sequence 2, Appl1
41	83.5	6.7	429	3	PCT-US93-02024-2	Sequence 2, Appl1
42	83.5	6.7	671	3	US-09-121-321-16	Sequence 16, Appl1
43	83.5	6.7	671	4	US-08-933-803A-16	Sequence 16, Appl1
44	83	6.7	28	5	PCT-US94-05150-12	Sequence 12, Appl1
45	83	6.7	758	1	US-07-756-250-16	Sequence 16, Appl1

## ALIGNMENTS

RESULT 1  
US-08-243-545-6  
Sequence 6, Application US/08243545  
Patent No. 5554512  
GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESS: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER REABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/243,545  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.7e-117;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDDLQDYPTV 60  
DB 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDDLQDYPTV 60  
DB 61 ASNLODELCGLMRVLAQRMERLKTAVGSKMOGLLEVRNTEIHVTKCAFGPPSCL 120  
QY 121 RFVQTNISRLQETSEQVLAKPWITRONFSRCLELCQPDSSSTLPPWSPRPLEATAPT 180  
DB 121 RFVQTNISRLQETSEQVLAKPWITRONFSRCLELCQPDSSSTLPPWSPRPLEATAPT 180  
QY 181 APQPLLILLLLPVGLLLAAACLHMQRTRRRTPRGEQVPVPSPQDLLLVEH 235  
DB 181 APQPLLILLLLPVGLLLAAACLHMQRTRRRTPRGEQVPVPSPQDLLLVEH 235

## RESULT 2

US-08-993-962-6  
Sequence 6, Application US/08993962  
Patent No. 5843423

GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,962  
FILING DATE: December 18, 1993

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,407  
FILING DATE: December 3, 1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.7e-117;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDDLQDYPTV 60  
DB 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDDLQDYPTV 60  
DB 61 ASNLODELCGLMRVLAQRMERLKTAVGSKMOGLLEVRNTEIHVTKCAFGPPSCL 120  
QY 121 RFVQTNISRLQETSEQVLAKPWITRONFSRCLELCQPDSSSTLPPWSPRPLEATAPT 180  
DB 121 RFVQTNISRLQETSEQVLAKPWITRONFSRCLELCQPDSSSTLPPWSPRPLEATAPT 180  
QY 181 APQPLLILLLLPVGLLLAAACLHMQRTRRRTPRGEQVPVPSPQDLLLVEH 235  
DB 181 APQPLLILLLLPVGLLLAAACLHMQRTRRRTPRGEQVPVPSPQDLLLVEH 235

## RESULT 3

US-09-160-841-6  
Sequence 6, Application US/09160841  
Patent No. 6190655

GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/160,841  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,407  
FILING DATE: December 3, 1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-160-841-6

Query Match 100.0%; Score 1242; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.7e-117;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLLSSGSLGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
DB 1 MTVLAPAMSPPTYYLLLLLLSSGSLGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
QY 61 ASNQDELGCGLMRLVLAQRMERLKTVAAGSKMOGLLERNTETIHFTKCAFPSPSCL 120  
DB 61 ASNQDELGCGLMRLVLAQRMERLKTVAAGSKMOGLLERNTETIHFTKCAFPSPSCL 120  
QY 121 RFVOTNISRLQETSEQLVALKPMITRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180  
DB 121 RFVOTNISRLQETSEQLVALKPMITRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180  
QY 181 APOPLLILLLLPVGLLLLAAMCLHMQRRRTPRGEQVPVPSPQDLLVEH 235  
DB 181 APOPLLILLLLPVGLLLLAAMCLHMQRRRTPRGEQVPVPSPQDLLVEH 235

RESULT 4  
US-09-109-100-1  
Sequence 1, Application us/09109100C  
Patent No. 6291661  
GENERAL INFORMATION:  
APPLICANT: McGrew, Jeffrey T.  
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
FILE REFERENCE: 03260.0028  
CURRENT APPLICATION NUMBER: US/09/109,100C  
CURRENT FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-109-100-1

Query Match 100.0%; Score 1242; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.7e-117;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLLSSGSLGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
DB 1 MTVLAPAMSPPTYYLLLLLLSSGSLGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
QY 61 ASNQDELGCGLMRLVLAQRMERLKTVAAGSKMOGLLERNTETIHFTKCAFPSPSCL 120  
DB 61 ASNQDELGCGLMRLVLAQRMERLKTVAAGSKMOGLLERNTETIHFTKCAFPSPSCL 120  
QY 121 RFVOTNISRLQETSEQLVALKPMITRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180  
DB 121 RFVOTNISRLQETSEQLVALKPMITRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180  
QY 181 APOPLLILLLLPVGLLLLAAMCLHMQRRRTPRGEQVPVPSPQDLLVEH 235  
DB 181 APOPLLILLLLPVGLLLLAAMCLHMQRRRTPRGEQVPVPSPQDLLVEH 235

RESULT 5  
PCT-US94-05365-6  
Sequence 6, Application PC/TUS9405365  
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for FLT3/FLK-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05365  
FILING DATE: May 24, 1994  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: -to be assigned-  
FILING DATE: May 11, 1994  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/209,502  
FILING DATE: March 7, 1994  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,407  
FILING DATE: December 3, 1993  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-05365-6

Query Match 100.0%; Score 1242; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.7e-117;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLLSSGSLGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
DB 1 MTVLAPAMSPPTYYLLLLLLSSGSLGTQDCSFQHSPISSDPAVKIRELSYLLQDYPTV 60  
QY 61 ASNQDELGCGLMRLVLAQRMERLKTVAAGSKMOGLLERNTETIHFTKCAFPSPSCL 120  
DB 61 ASNQDELGCGLMRLVLAQRMERLKTVAAGSKMOGLLERNTETIHFTKCAFPSPSCL 120  
QY 121 RFVOTNISRLQETSEQLVALKPMITRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180

Db 121 RFQVQISRLLOETSEQLVAKLPMITRONSRLQCCOPDSSSTLPSPRPLEATAPIT 180  
OY 181 APOPLLVLVGLLLAAAMCLHMORTRRRTPRGEOVPPVPSODLLVEH 235  
Db 181 APOPLLVLVGLLLAAAMCLHMORTRRRTPRGEOVPPVPSODLLVEH 235

## RESULT 6

US-09-109-100-10  
; Sequence 10, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:  
; APPLICANT: Gradadis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/109,100C  
; CURRENT FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-109-100-10

Query Match 90.5%; Score 1124; DB 4; Length 212;  
Best Local Similarity 100.0%; Pred. No. 1.2e-105;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 SCQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRLVLAQRMERL 84  
Db 2 SCQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRLVLAQRMERL 61  
OY 85 RLKTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLRFVQVOTNISRLQETSEQLVAKPM 144  
Db 62 RLKTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLRFVQVOTNISRLQETSEQLVAKPM 121  
OY 145 ITRONFSRCLQCCOPDSSSTLPSPRPLEATAPAPQPLLVLVGLLLAAAMC 204  
Db 122 ITRONFSRCLQCCOPDSSSTLPSPRPLEATAPAPQPLLVLVGLLLAAAMC 181  
OY 205 LHMORTRRRTPRGEOVPPVPSODLLVEH 235  
Db 182 LHMORTRRRTPRGEOVPPVPSODLLVEH 212

## RESULT 7

US-09-109-100-18  
; Sequence 18, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:  
; APPLICANT: Gradadis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/109,100C  
; CURRENT FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-109-100-18

Query Match 89.7%; Score 1114; DB 4; Length 209;  
Best Local Similarity 100.0%; Pred. No. 1.2e-104;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRLVLAQRMERL 86  
Db 181 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRLVLAQRMERL 86

Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRLVLAQRMERL 60  
OY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLRFVQVOTNISRLQETSEQLVAKPMIT 146  
Db 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLRFVQVOTNISRLQETSEQLVAKPMIT 120  
OY 147 RONSRLQCCOPDSSSTLPSPRPLEATAPAPQPLLVLVGLLLAAAMC 206  
Db 121 RONSRLQCCOPDSSSTLPSPRPLEATAPAPQPLLVLVGLLLAAAMC 180  
OY 207 MORTRRRTPRGEOVPPVPSODLLVEH 235  
Db 181 MORTRRRTPRGEOVPPVPSODLLVEH 209

## RESULT 8

US-09-109-100-9  
; Sequence 9, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:  
; APPLICANT: Gradadis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/109,100C  
; CURRENT FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-109-100-9

Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 3e-104;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRLVLAQRMERL 86  
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRLVLAQRMERL 60  
OY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLRFVQVOTNISRLQETSEQLVAKPMIT 146  
Db 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRLRFVQVOTNISRLQETSEQLVAKPMIT 120  
OY 147 RONSRLQCCOPDSSSTLPSPRPLEATAPAPQPLLVLVGLLLAAAMC 206  
Db 121 RONSRLQCCOPDSSSTLPSPRPLEATAPAPQPLLVLVGLLLAAAMC 180  
OY 207 MORTRRRTPRGEOVPPVPSODLLVEH 235  
Db 181 MORTRRRTPRGEOVPPVPSODLLVEH 209

## RESULT 9

US-09-109-100-12  
; Sequence 12, Application US/09109100C  
; Patent No. 6291661  
; GENERAL INFORMATION:  
; APPLICANT: Gradadis, Thomas J.  
; APPLICANT: McGrew, Jeffrey T.  
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
; FILE REFERENCE: 03260.0028  
; CURRENT APPLICATION NUMBER: US/09/109,100C  
; CURRENT FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-109-100-12

Query Match 89.7%; Score 1114; DB 4; Length 209;  
Best Local Similarity 100.0%; Pred. No. 1.2e-104;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RESULT 11  
US-09-109-100-17  
Sequence 17, Application US/09109100C  
Patent No. 6291661  
GENERAL INFORMATION:  
APPLICANT: Graddis, Thomas J.  
TITLE OF INVENTION: FIT3-L MUTANTS AND METHODS OF USE  
FILE REFERENCE: 03260.0028  
CURRENT APPLICATION NUMBER: US/09/109.100C  
CURRENT FILING DATE: 1998-07-02

RESULT 13  
US-09-109-100-15  
; Sequence 15, Application US/09109100C  
; Patent No. 6291661



GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:26:11 ; Search time 34 Seconds  
(without alignments)  
1424.149 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242  
Sequence: 1 MTVLAPAWSPTTYLLLLLL.....RCEQVPVPSQDLLLVEH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertibrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	895.5	72.1	294	6	09MZV0	09MZV0 canis famli
2	894.5	72.0	291	6	09MZU9	09MZU9 felis silve
3	840	67.6	232	6	09GKE0	09GKE0 bos taurus
4	835	67.2	292	6	08NMW1	08NMW1 bos taurus
5	746	60.1	274	6	09GRD9	09GRD9 bos taurus
6	602.5	48.5	172	11	061104	061104 mus musculu
7	578	46.5	169	11	08VCH4	08VCH4 mus musculu
8	112.5	9.1	579	10	09LGC8	09LGC8 oryza sativ
9	104.5	8.4	668	5	09GY11	09GY11 leishmania
10	102.5	8.3	648	5	09GY33	09GY33 leishmania
11	100.5	8.1	1809	11	08VIM6	08VIM6 mus musculu
12	98.5	7.9	345	5	09N753	09N753 leishmania
13	95.5	7.7	1240	12	09DMH8	09DMH8 rat cytoome
14	93.5	7.5	658	10	09C5T0	09C5T0 arabidopsis
15	93	7.5	1217	5	017889	017889 caenorhabdi
16	92.5	7.4	387	11	08VD70	08VD70 mus musculu

17	92.5	7.4	560	5	09GYA1	09GYA1 leishmania
18	92.5	7.4	1400	5	08SZS7	08SZS7 drosophila
19	92	7.4	251	4	09HAD2	09HAD2 homo sapien
20	90.5	7.3	536	5	09GYA0	09GYA0 leishmania
21	90.5	7.3	660	5	09GY15	09GY15 leishmania
22	90.5	7.3	5120	13	09PU36	09PU36 gallus gall
23	89.5	7.2	474	5	017610	017610 caenorhabdi
24	88.5	7.1	238	16	08VWX3	08VWX3 anabaena sp
25	88.5	7.1	270	4	09UMT1	09UMT1 homo sapien
26	88.5	7.1	404	10	09AMJ4	09AMJ4 oryza sativ
27	88.5	7.1	1267	10	09AJD5	09AJD5 oryza sativ
28	88.5	7.1	1386	4	075064	075064 homo sapien
29	88	7.1	250	6	09GKE2	09GKE2 sus scrofa
30	88	7.1	675	11	09DPT2	09DPT2 mus musculu
31	88	7.1	753	12	056971	056971 kennedy ye
32	87.5	7.0	470	10	09LUI1	09LUI1 arabidopsis
33	87.5	7.0	946	10	022015	022015 cyllindrothe
34	87	7.0	510	5	044018	044018 leishmania
35	87	7.0	5317	5	08TA74	08TA74 hemilecentrot
36	86.5	6.9	255	11	09OJ33	09OJ33 mus musculu
37	86.5	6.9	299	6	09TTT9	09TTT9 bos taurus
38	86	6.9	289	12	08A647	08A647 parametium
39	86	6.9	706	5	023600	023600 caenorhabdi
40	86	6.9	911	11	035407	035407 mus musculu
41	85.5	6.9	795	5	095U02	095U02 toxoplasma
42	85	6.8	282	4	09BSA1	09BSA1 homo sapien
43	85	6.8	289	16	09A3K1	09A3K1 caulobacter
44	85	6.8	413	11	09GWM1	09GWM1 mus musculu
45	85	6.8	1217	4	09P2D0	09P2D0 homo sapien

## ALIGNMENTS

### RESULT 1

ID 09MZV0 PRELIMINARY; PRT; 294 AA.  
AC 09MZV0;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Fil3 ligand.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP MEDLINE=20358731; PubMed=10902925;  
RA Yang S., Sim G.K.;  
RT "Molecular cloning of canine and feline fil3 ligand reveals hgh  
RT degree of similarity to the human and mouse homologue but uniquely  
RL long cytoplasmic domain";  
RL DNA Seq. 11:163-166(2000).  
DR EMBL; AF15148; AAF87088.1;  
DR InterPro; IPR004213; Fil3\_lig.  
DR Pfam; PFO2947; Fil3\_lig. 1.  
SQ SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;

Query Match 72.1%; Score 895.5; DB 6; Length 294;  
Best Local Similarity 77.1%; Pred. No. 3.5e-80;  
Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;  
QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGVDCSFOFSPISSDPAVVKIRELSVDLLDYPYTV 60  
DB 1 MIVLAPAWSPTASLLLLLLSPGLRGTPDCSFSHSSTSTRAVTIRKLSLDLDDYPTV 60  
QY 61 ASNLODEELCGRLVLAQRMERLKTVAASKMKGLELVNTEIHFVTKCAFOPPSCL 120  
DB 61 ASNLODEELCGAFRLVLAQRMWRLOAVAGSQMQLLEAVNTEIHVTFARFPLPSCL 120  
QY 121 RFVQTNISRLLOETSEDLVALKPWITTRONFSRCLDELQCPDSSYLPWPMSRPLEAAPT 180  
||||||| |||:||||| ||||||||| ||||||||| ||| |||



Q9G6D9 :  
 ID 09GKD9 PRELIMINARY; PRT; 274 AA.  
 AC 09GKD9  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Flt3 ligand isoform-2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20570936; PubMed=11120823;  
 RA Mwangi W., Brown W.C., Palmer G.H.:  
 RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain  
 RT required for receptor binding and function using naturally occurring  
 RT ligand isoforms."  
 RL J. Immunol. 165:6966-6974(2000).  
 DR EMBL; AF282986; AAF9323.1; -.  
 DR InterPro: IPR004213; Flt3\_1lg.  
 DR Pfam: PF02947; flt3\_1lg; 1.  
 DR SEQUENCE 274 AA; 30372 MW; 725A7E77A95DA98B CRC64;  
 SQ  
 Query Match 60.1%; Score 746; DB 6; Length 274;  
 Best Local Similarity 69.6%; Pred. No. 1.8e-65;  
 Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;  
 QY 1 MTVALPAPMSPT-TYLLLLLSGLSGTQDCSFQHSPISSPFAVKIRELSYLLQDYPT 59  
 DB 1 MTVALPAPMSPTSLLLLLLSPLCLRGTPDCYFSHSPISSNFKYKFRRLTDLKLDYPT 60  
 QY 60 VASNLQDEELCGGLRWLVLAORWMEKRLKTVAGSKMKGLELVNTEIHFVTCARFQPPSC 119  
 DB 61 VASNLQDEKCKALMSLFLAORWIEQLKTVAGSKMKGLELVNTEIHFVTCARFQPPSC 114  
 QY 120 LRFVQTNISRLQETSEQLVAKPWITR--QNFSCLELQCCPDSSTLPPEWSPRLATAP 179  
 DB 115 -----QDTHQQLKALKPWITRNFSCLELQCCPDSSTLPPEWSPRLATAP 162  
 QY 180 TAPQPP---LLLLLLPVGLLLLAANCLHWQTRRRRRPRGEG 220  
 DB 163 PGFSPLLLLLLLLLPVALLLATAMWLCRWRRRRRRTRPRGER 206  
 RESULT 6  
 061104  
 ID 061104 PRELIMINARY; PRT; 172 AA.  
 AC 061104;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Flt3 ligand, T169 form.  
 GN Flt3L.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,  
 RA Matsson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G., Rosnet O.,  
 RA Blumberg P.M., Hannum C.:  
 RT "Flt3 ligand: expression, genomic organization, alternatively spliced  
 RT forms and processing."  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U44024; AAA93305.1; -.  
 DR MGD; MGI:95560; Flt3L.  
 DR InterPro: IPR004213; Flt3\_1lg.  
 DR InterPro: IPR001230; Prey1\_site.  
 DR Pfam: PF02947; flt3\_1lg; 1.  
 DR PROSITE; PS00294; PRENITATION; UNKNOWN\_1.

SQ SEQUENCE 172 AA; 19465 MW; 04F0A010171E3384 CRC64;  
 Query Match 48.5%; Score 602.5; DB 11; Length 172;  
 Best Local Similarity 72.6%; Pred. No. 1.5e-51;  
 Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2;  
 QY 1 MTVALPAPMSPT-TYLLLLLSGLSGTQDCSFQHSPISSPFAVKIRELSYLLQDYPT 59  
 DB 1 MTVALPAPMSPTSLLLLLLSPLCLRGTPDCYFSHSPISSNFKYKFRRLTDLKLDYPT 60  
 QY 60 VASNLQDEELCGGLRWLVLAORWMEKRLKTVAGSKMKGLELVNTEIHFVTCARFQPPSC 119  
 DB 61 VASNLQDEKCKALMSLFLAORWIEQLKTVAGSKMKGLELVNTEIHFVTCARFQPPSC 120  
 QY 120 LRFVQTNISRLQETSEQLVAKPWITR--QNFSCLELQCCPDSSTLPPEWSPRLATAP 175  
 DB 121 LRFVQTNISRLQETSEQLVAKPWITR--QNFSCLELQCCPDSSTLPPEWSPRLATAP 168  
 RESULT 7  
 08VCH4  
 ID 08VCH4 PRELIMINARY; PRT; 169 AA.  
 AC 08VCH4;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Similar to FMS-like tyrosine kinase 3 ligand.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER.  
 RA Strausberg R.:  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019801; AAH19801.1; -.  
 DR InterPro: IPR004213; Flt3\_1lg.  
 DR Pfam: PF02947; flt3\_1lg; 1.  
 DR KW Kinase.  
 SQ SEQUENCE 169 AA; 18986 MW; 5B4CA47D9724EFP2 CRC64;  
 Query Match 46.5%; Score 578; DB 11; Length 169;  
 Best Local Similarity 68.6%; Pred. No. 3.7e-49;  
 Matches 120; Conservative 14; Mismatches 29; Indels 12; Gaps 3;  
 QY 1 MTVALPAPMSPT-TYLLLLLSGLSGTQDCSFQHSPISSPFAVKIRELSYLLQDYPT 59  
 DB 1 MTVALPAPMSPTSLLLLLLSPLCLRGTPDCYFSHSPISSNFKYKFRRLTDLKLDYPT 60  
 QY 60 VASNLQDEELCGGLRWLVLAORWMEKRLKTVAGSKMKGLELVNTEIHFVTCARFQPPSC 119  
 DB 61 VASNLQDEKCKALMSLFLAORWIEQLKTVAGSKMKGLELVNTEIHFVTCARFQPPSC 120  
 QY 120 LRFVQTNISRLQETSEQLVAKPWITR--QNFSCLELQCCPDSSTLPPEWSPRLATAP 172  
 DB 121 LRFVQTNISRLQETSEQLVAKPWITR--QNFSCLELQCCPDSSTLPPEWSPRLATAP 166  
 RESULT 8  
 09LGC8  
 ID 09LGC8 PRELIMINARY; PRT; 579 AA.  
 AC 09LGC8;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Putative extensin-like protein.  
 GN P0406H10.6 OR OJ1174\_D05.5.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriatoidae; Oryzae; Oryza.  
 NCBI\_TaxID=4530;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
 RT clone: P0406H10."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC  
 RT clone: O01174\_D05."  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP002524; BAB07956.1; -  
 DR EMBL: AP003118; BAB33013.1; -  
 DR InterPro: IPR001611; LRR-  
 DR InterPro: IPR003592; LRR\_out.  
 DR InterPro: IPR002965; P\_rich\_extensn.  
 DR Pfam: PF00560; LRR\_6.  
 DR PRINTS: PRO1582; KV33CHANNEL.  
 DR PRINTS: PRO1217; PRICHEXTENSN.  
 DR SMART: SM00370; LRR\_5.  
 DR PROSITE: PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
 SQ SEQUENCE 579 AA; 62607 MW; 04457E18E7405AAF CRC64;

Query Match 9.1%; Score 112.5; DB 10; Length 579;  
 Best Local Similarity 23.7%; Pred. No. 0.013;  
 Matches 54; Conservative 28; Mismatches 69; Indels 77; Gaps 11;

QY 17 LLLLSGLSGTDCSFQHSPISSDFPAVKIRELSLDYLLQDYPTVASNLQDEELCGGLMRL 76  
 DB 244 ILINGLG-----SCLPEVGM-LREIVTF-----DVSNRLAGPLPSA 282  
 OY 77 VLAQRMWERLKTVAAGSMOGLERVNTIEHFVTKCAFO-----PPPSCLRFV-----QT 125  
 DB 283 VAGMKRVEQL-DVAHNILITAIQAVCELPRLNFTFAVYFGEPPSCAHANPRVYDRR 341  
 OY 126 NI--SRLLQTSFQVLAALKWITRONFSR-----CLELQCPDSSSTLPSPSPRLXATAP 179  
 DB 342 NCLPBNPAQFTLRQCAAF-----FARPPVNCAMFQCKFPVAPALPPSPPP--SPP 391  
 OY 180 TAQPPPLLLLLPVGLLLAAMCLHMORTRRRTPRRGQVPPVSP 227  
 DB 392 PSPPP-----SPPSPSTSPPPSP 411  
 RESULT 9  
 Q9GY11 PRELIMINARY; PRT; 668 AA.  
 AC Q9GY11;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Probable surface antigen p2.  
 GN LM12.156.  
 GN Leishmania major.  
 OS Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OC NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRIEDLIN;  
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL390114; CAC02038.2; -  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001611; LRR-  
 DR InterPro: IPR002965; P\_rich\_extensn.  
 DR Pfam: PF00560; LRR\_6.  
 DR PRINTS: PRO1217; PRICHEXTENSN.  
 DR SMART: SM0181; EGF\_1.

SQ SEQUENCE 668 AA; 70725 MW; CEB3ECAABC490C94 CRC64;

Query Match 8.4%; Score 104.5; DB 5; Length 668;  
 Best Local Similarity 26.6%; Pred. No. 0.093;  
 Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;

QY 4 LAPWSPFTYLLLLLLSSGSLGTDCSFQHSPISSDFPAVKIRELSLDYLLQDYPTVASN 63  
 DB 149 LPPEWSSMPNLQTLQVRLKLSGT-----LPADWS-SLKSLSNVLEDPIT----- 194  
 OY 64 LDPELQGLMRLVLAQRMWERLKTVAAGSMOGLERVNTIEHFVTKCAFOPP-----S 118  
 DB 195 -----GL-----LPPEW-----GSLERIQQLVRLKLTGRLPPQSPMK 229  
 QY 119 CLRFOV---TNISRLQ-----ETSEQLVALKP-WITRONFSRCLQLQCP 160  
 DB 230 ALRFLTLDTGNTLSGTLPPQWSAMASYISLNLTEGTEVSGTLPPKWSMSRL-QTLNLRRTK 288  
 OY 161 DSSTLPPEWSR-----PLEATAPTAPOP-----LLLLLLPVGLL--LLAAM 203  
 DB 289 VSGTLPEWSSMGSANLQSLTQVSGTLPPQWSMKKLTQLLTDTLLSGTLPAEM 345

RESULT 10

Q9GY33 PRELIMINARY; PRT; 648 AA.  
 AC Q9GY33;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Probable surface antigen p2.  
 GN LM12.121.  
 GN Leishmania major.  
 OS Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OC NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRIEDLIN;  
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL390114; CAC02017.2; -  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001611; LRR-  
 DR InterPro: IPR002965; P\_rich\_extensn.  
 DR Pfam: PF00560; LRR\_7.  
 DR PRINTS: PRO1217; PRICHEXTENSN.  
 DR SMART: SM0181; EGF\_1.  
 SQ SEQUENCE 648 AA; 68470 MW; 8EB78AC101E01286 CRC64;

Query Match 8.3%; Score 102.5; DB 5; Length 648;  
 Best Local Similarity 26.6%; Pred. No. 0.14;  
 Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;

QY 4 LAPWSPFTYLLLLLLSSGSLGTDCSFQHSPISSDFPAVKIRELSLDYLLQDYPTVASN 63  
 DB 149 LPPEWSSMPNLVLAQRMWERLKTVAAGSMOGLERVNTIEHFVTKCAFOPP-----S 118  
 OY 64 LDPELQGLMRLVLAQRMWERLKTVAAGSMOGLERVNTIEHFVTKCAFOPP-----S 118  
 DB 195 -----GL-----LPPEW-----GSLERIQQLVRLKLTGRLPPQSPMK 229  
 QY 119 CLRFOV---TNISRLQ-----ETSEQLVALKP-WITRONFSRCLQLQCP 160  
 DB 230 ALRFLTLDTGNTLSGTLPPQWSAMASYISLNLTEGTEVSGTLPPKWSMSRL-QTLNLRRTK 288  
 OY 161 DSSTLPPEWSR-----PLEATAPTAPOP-----LLLLLLPVGLL--LLAAM 203  
 DB 289 VSGTLPEWSSMGSANLQSLTQVSGTLPPQWSMKKLTQLLTDTLLSGTLPAEM 345

RESULT 11

OBVTM6

ID 08VIM6 PRELIMINARY; PRT: 1809 AA.  
 AC 08VIM6;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Stereocilin.  
 GN STRC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX MEDLINE=11687802;  
 RA STRAIN=BALE/C;  
 RA Verpey E., Masmondi S., Zwaenepoel I., Leibovici M., Hutchin T.P.,  
 RA Del Castillo I., Nouaille S., Blanchard S., Laine S., Popot J.L.,  
 RA Moreno F., Mueller R.F., Petit C.;  
 RT "Mutations in a new gene encoding a protein of the hair bundle cause  
 RT non-syndromic deafness at the DFNB16 locus."  
 RL Nat. Genet. 29:345-349(2001).  
 DR EMBL: AF375593; AAL35321.1; -  
 DR MGD: MGI:2153816; Strc  
 SO SEQUENCE 1809 AA; 196404 MW; 012382C9E80EC825 CRC64;  
 Query Match 8.1%; Score 100.5; DB 11; Length 1809;  
 Best Local Similarity 23.7%; Pred. No. 0.74;  
 Matches 70; Conservative 25; Mismatches 93; Indels 107; Gaps 14;  
 QY 3 VLAWMSFTYLL-----LLLL-----SSGLSGTDCSFHSPISDFAVKIRE 47  
 DB 168 VLADWLPSTLMLLEGRWQALVOLQPSVDPNTATGIDG-----RE 208  
 QY 48 LSDVLDDY--PVTVASNLQDEE-ICGSLMRLV---LAQRMERLKV----- 89  
 DB 209 PAHFLOGGLGLTPAGELGESEALMGGLRTYGAFLYAAQEGELRTHSLQDEVESIM 268  
 QY 90 -----AGSKMGLLERVNTEIHFTK-----AFOPPSCLRFVOTNISRL 131  
 DB 269 GQPPDASGCGGCGNLOQLLMGMRNLSMDARALGFLSGSPPPALLHCLSRGV--L 326  
 QY 132 QETSEQLVAKPWITTRQNSFSCLELOCOPDSSTLPP-----PMSPPLE 175  
 DB 327 PRASQPAHAHISP---RORRAISVEALCENHSGPEPPYSISNFSYLLCOHAKPAPRPP 383  
 QY 176 AT---APTAPQPLLLLLLPVGLLLAAACLMQRTRRTPRGEQVP--PVPS 226  
 DB 384 TTPRPPPTTPPPPTTPTTPIP-----DTTQPPVTPRPPPTTTPPPPS 426  
 RESULT 12  
 Q9N753 PRELIMINARY; PRT: 345 AA.  
 AC Q9N753;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Probable surface antigen p2.  
 GN LM12.08.  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 NCBI\_TaxID=5664;  
 RX MEDLINE=5664;  
 RA STRAIN=FRIEDLIN;  
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Bartell B.,  
 RA Oliver K.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL390114; CAB98658.2; -  
 DR InterPro: IPR001611; LRR  
 DR InterPro: IPR003592; LRR-out.  
 DR Pfam: Pf00560; LRR: 3.  
 DR SMART: SM00370; LRR: 3.

SO SEQUENCE 345 AA; 37530 MW; 06ECC850B1B54B70 CRC64;  
 Query Match 7.9%; Score 98.5; DB 5; Length 345;  
 Best Local Similarity 23.8%; Pred. No. 0.17;  
 Matches 56; Conservative 21; Mismatches 57; Indels 101; Gaps 10;  
 QY 6 PAWSFTYLLLLLLLSGLSGT-----QDCSFHSPISDFAVKIRELS 49  
 DB 152 PEMWSMTLSVLNLRGTISGTLPPQWGMKARSLQDQDSSLSMSAI----- 205  
 QY 50 DYLLQDFVTVASNLQDEELG-----GLMRLVLAQRMERLKVAGSKMGLLERVTE 104  
 DB 206 -----PMLASVSLKGNKFGVCRTGIRRLVL--WTSRSTRATA----- 245  
 QY 105 IHFTKCAFOP--PPSCLRVOTNISRLQETSQVALKAPWITRQNSFSCLELOCOPD 161  
 DB 246 --WLKRTQRPPLSPPPQRPRTSLT-----FPLRRGPR 278  
 QY 162 SSTLPPSPPLLEATAPAPQPLLL-----LTPVGLLLAAACLMQRTRR 212  
 DB 279 LSRLPQPALRRRLN-----PQPLRRRLNRPRLP-----QOTRR 313  
 RESULT 13  
 Q9DMH8 PRELIMINARY; PRT: 1240 AA.  
 AC Q9DMH8;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Pr2.  
 GN R2.  
 OS Rat cytomegalovirus (strain Mastricht).  
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 CC Betaherpesvirinae; Muromegalovirus.  
 NCBI\_TaxID=79700;  
 RX MEDLINE=10906222;  
 RA STRAIN=MASTRICHT;  
 RA Vink C., Beuken E., Bruggeman C.A.;  
 RT "Complete DNA sequence of the rat cytomegalovirus genome."  
 RL J. Virol. 74:7656-7665(2000).  
 RN 121  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MASTRICHT;  
 RX MEDLINE=20473137; PubMed=11018281;  
 RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A.;  
 RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a  
 RT spliced transcript."  
 RL Virus Res. 69:119-130(2000).  
 DR EMBL: AF232689; AAF99111.1; -  
 SO SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;  
 Query Match 7.7%; Score 95.5; DB 12; Length 1240;  
 Best Local Similarity 33.0%; Pred. No. 1.5;  
 Matches 29; Conservative 8; Mismatches 18; Indels 33; Gaps 5;  
 QY 160 PDSSTL-----PPWSPPR--LEATAPAPOP-PLLLLLLPVGLLLAA 201  
 DB 1060 PDSSTAVTGEATTERSTPATEPRPRPLPGVDSALPLAPQPTLLSLVPA----- 1112  
 QY 202 AMCLHMORTRRTPRPPGEQVPVPSPOD 229  
 DB 1113 -----QATRASPRPETDAP-PTPAD 1132  
 RESULT 14  
 Q9C5T0 PRELIMINARY; PRT: 658 AA.  
 AC Q9C5T0;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)





GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:28:06 ; Search time 57 Seconds  
(without alignments)  
408.870 Million cell updates/sec

Title: US-08-994-468-6  
Perfect score: 1242  
Sequence: 1 MVLAPAMSPRTYLLLL...RPGEQVPPVSPDLLLVEH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB pep:\*\n2: /cgn2\_6/ptodata/2/pubppaa/PCF\_NEW\_PUB pep:\*\n3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB pep:\*\n4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB pep:\*\n5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB pep:\*\n6: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB pep:\*\n7: /cgn2\_6/ptodata/2/pubppaa/PCFUS\_PUBCOMB pep:\*\n8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB pep:\*\n9: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB pep:\*\n10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB pep:\*\n11: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB pep:\*\n12: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB pep:\*\n13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB pep:\*\n14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1242	100.0	235	9 US-10-095-449-6	Sequence 6, Appl1
2	1242	100.0	235	10 US-09-448-378-1	Sequence 1, Appl1
3	1242	100.0	235	10 US-09-983-806-6	Sequence 6, Appl1
4	1242	100.0	235	10 US-09-904-536-1	Sequence 1, Appl1
5	1124	90.5	212	10 US-09-904-536-10	Sequence 10, Appl1
6	1114	89.7	209	10 US-09-904-536-18	Sequence 18, Appl1
7	1110	89.4	209	10 US-09-904-536-9	Sequence 9, Appl1
8	1110	89.4	209	10 US-09-904-536-12	Sequence 12, Appl1
9	1110	89.4	209	10 US-09-904-536-14	Sequence 14, Appl1
10	1110	89.2	209	10 US-09-904-536-17	Sequence 17, Appl1
11	1108	89.2	209	10 US-09-904-536-11	Sequence 11, Appl1
12	1108	89.2	209	10 US-09-904-536-15	Sequence 15, Appl1
13	1107	89.1	209	10 US-09-904-536-13	Sequence 13, Appl1
14	1106	89.0	209	10 US-09-904-536-8	Sequence 8, Appl1
15	1100	88.6	209	10 US-09-904-536-16	Sequence 16, Appl1
16	822	66.2	156	9 US-10-053-355A-1	Sequence 1, Appl1
17	768.5	61.9	231	9 US-10-095-449-2	Sequence 2, Appl1
18	768.5	61.9	231	10 US-09-448-378-2	Sequence 2, Appl1
19	768.5	61.9	231	10 US-09-983-806-2	Sequence 2, Appl1

20	506.5	40.8	137	10 US-09-904-536-19	Sequence 19, Appl1
21	91.5	7.4	674	10 US-09-899-471-2	Sequence 2, Appl1
22	91.5	7.4	698	9 US-09-866-050A-509	Sequence 509, App
23	91.5	7.4	698	9 US-09-863-818A-8	Sequence 8, Appl1
24	91.5	7.4	698	10 US-09-899-471-5	Sequence 5, Appl1
25	89.5	7.2	874	10 US-09-826-508-26	Sequence 26, Appl1
26	89.5	7.2	941	9 US-09-793-139-47	Sequence 47, Appl1
27	89.5	7.2	941	9 US-10-300-616-31	Sequence 31, Appl1
28	89.5	7.2	941	10 US-09-818-879-47	Sequence 47, Appl1
29	89.5	7.2	941	10 US-09-211-755B-47	Sequence 47, Appl1
30	88.5	7.1	1257	9 US-10-109-324-2	Sequence 2, Appl1
31	88	7.1	238	9 US-10-174-363-30	Sequence 30, Appl1
32	87.5	7.0	415	9 US-09-917-372-20	Sequence 20, Appl1
33	87.5	7.0	415	10 US-09-826-512-6	Sequence 6, Appl1
34	87.5	7.0	415	10 US-09-925-300-1680	Sequence 1680, App
35	87.5	7.0	415	10 US-09-935-727-8	Sequence 8, Appl1
36	87.5	7.0	479	9 US-10-108-605-57	Sequence 57, Appl1
37	87.5	7.0	570	9 US-09-991-496-104	Sequence 104, App
38	87.5	7.0	570	10 US-09-874-923-104	Sequence 104, App
39	85.5	6.9	519	10 US-09-925-300-1680	Sequence 1680, App
40	84.5	6.8	610	10 US-09-783-708-1	Sequence 1, Appl1
41	84.5	6.8	913	10 US-09-223-490-4	Sequence 4, Appl1
42	84.5	6.8	1134	9 US-10-001-873-50	Sequence 50, Appl1
43	84	6.8	107	10 US-09-220-920-52	Sequence 52, Appl1
44	84	6.8	220	9 US-10-001-054-56	Sequence 56, Appl1
45	84	6.8	220	10 US-09-220-920-26	Sequence 26, Appl1

## ALIGNMENTS

RESULT 1  
US-10-095-449-6  
Sequence 6, Application US/10095449  
Patent No. US20020160004A1  
GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/095,449  
FILING DATE: 13-Mar-2002  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/669,692  
FILING DATE: 24-JUN-1996  
APPLICATION NUMBER: US/08/162,407  
FILING DATE: December 3, 1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-095-449-6

Query Match 100.0%; Score 1242; DB 9; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.4e-101;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSLGTFQDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60  
DB 1 MTVALPAMSPPTTYLLLLSSGSLGTFQDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60  
QY 61 ASNLQDEELCGGLMRVLVLAQRMERLKTAVGSKMGLLEEVNTEIHFVTKCAEQPPPSCL 120  
DB 61 ASNLQDEELCGGLMRVLVLAQRMERLKTAVGSKMGLLEEVNTEIHFVTKCAEQPPPSCL 120  
QY 121 RFVQNTISRLLQETSEQLVALKPWITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPT 180  
DB 121 RFVQNTISRLLQETSEQLVALKPWITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPT 180  
QY 181 APQPPILLLLLPVGLLLAAACLHMQRTRRRTPRPGEOVPPVPSQDILLVEH 235  
DB 181 APQPPILLLLLPVGLLLAAACLHMQRTRRRTPRPGEOVPPVPSQDILLVEH 235

RESULT 2  
US-09-448-378-1  
Sequence 1, Application US/09448378  
Patent No. US20020034517A1  
GENERAL INFORMATION:  
APPLICANT: Brasel, Kenneth  
TITLE OF INVENTION: Dendritic Cell Stimulatory Factor  
FILE REFERENCE: 2836-D  
CURRENT APPLICATION NUMBER: US/09/448,378  
CURRENT FILING DATE: 1999-11-23  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-448-378-1

Query Match 100.0%; Score 1242; DB 10; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.4e-101;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSLGTFQDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60  
DB 1 MTVALPAMSPPTTYLLLLSSGSLGTFQDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60  
QY 61 ASNLQDEELCGGLMRVLVLAQRMERLKTAVGSKMGLLEEVNTEIHFVTKCAEQPPPSCL 120  
DB 61 ASNLQDEELCGGLMRVLVLAQRMERLKTAVGSKMGLLEEVNTEIHFVTKCAEQPPPSCL 120  
QY 121 RFVQNTISRLLQETSEQLVALKPWITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPT 180  
DB 121 RFVQNTISRLLQETSEQLVALKPWITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPT 180  
QY 181 APQPPILLLLLPVGLLLAAACLHMQRTRRRTPRPGEOVPPVPSQDILLVEH 235  
DB 181 APQPPILLLLLPVGLLLAAACLHMQRTRRRTPRPGEOVPPVPSQDILLVEH 235

RESULT 3  
US-09-983-806-6

Sequence 6, Application US/09983806  
Patent No. US20020107365A1  
GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/983,806  
FILING DATE: 25-Oct-2001  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,626  
FILING DATE: 19-MAY-1995  
APPLICATION NUMBER: US 08/162,407  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-983-806-6

Query Match 100.0%; Score 1242; DB 10; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.4e-101;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSLGTFQDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60  
DB 1 MTVALPAMSPPTTYLLLLSSGSLGTFQDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60  
QY 61 ASNLQDEELCGGLMRVLVLAQRMERLKTAVGSKMGLLEEVNTEIHFVTKCAEQPPPSCL 120  
DB 61 ASNLQDEELCGGLMRVLVLAQRMERLKTAVGSKMGLLEEVNTEIHFVTKCAEQPPPSCL 120  
QY 121 RFVQNTISRLLQETSEQLVALKPWITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPT 180  
DB 121 RFVQNTISRLLQETSEQLVALKPWITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPT 180  
QY 181 APQPPILLLLLPVGLLLAAACLHMQRTRRRTPRPGEOVPPVPSQDILLVEH 235  
DB 181 APQPPILLLLLPVGLLLAAACLHMQRTRRRTPRPGEOVPPVPSQDILLVEH 235

RESULT 4

US-09-904-536-1  
: Sequence 1, Application US/09904536  
: Patent No. US20020111475A1  
: GENERAL INFORMATION:  
: APPLICANT: Graddis, Thomas J.  
: APPLICANT: McGrew, Jeffrey T.  
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
: FILE REFERENCE: 03260.0028  
: CURRENT APPLICATION NUMBER: US/09/904.536  
: CURRENT FILING DATE: 2001-07-16  
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
: PRIOR FILING DATE: 1999-07-02  
: NUMBER OF SEQ ID NOS: 20  
: SOFTWARE: PatentIn Ver. 2.1  
: SEQ ID NO 1  
: LENGTH: 235  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-904-536-1  
Query Match 100.0%; Score 1242; DB 10; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1,4e-101;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MTVLAPANSPTTYLLLLSSGSLGTDGCSFQHSPISSDFAVKIRELSYLLQDYPTV  
Qy 1 MTVLAPANSPTTYLLLLSSGSLGTDGCSFQHSPISSDFAVKIRELSYLLQDYPTV 60  
Db 1 MTVLAPANSPTTYLLLLSSGSLGTDGCSFQHSPISSDFAVKIRELSYLLQDYPTV 60  
Qy 61 ASNLODELCGGLMRLVLAQRMERLKTAVAGSKMGGLELERNTEHFVTKCAFQPPPSCL 120  
Db 61 ASNLODELCGGLMRLVLAQRMERLKTAVAGSKMGGLELERNTEHFVTKCAFQPPPSCL 120  
Qy 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLCLOCPDSSSTLPMPSPRLATAPT 180  
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLCLOCPDSSSTLPMPSPRLATAPT 180  
Qy 181 APOPELLLLLPVGLLLAAACMLHMORTRRRTRPRGEGVPPVSPDILLVEH 235  
Db 181 APOPELLLLLPVGLLLAAACMLHMORTRRRTRPRGEGVPPVSPDILLVEH 235  
RESULT 5  
US-09-904-536-10  
: Sequence 10, Application US/09904536  
: Patent No. US20020111475A1  
: GENERAL INFORMATION:  
: APPLICANT: Graddis, Thomas J.  
: APPLICANT: McGrew, Jeffrey T.  
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
: FILE REFERENCE: 03260.0028  
: CURRENT APPLICATION NUMBER: US/09/904.536  
: CURRENT FILING DATE: 2001-07-16  
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
: PRIOR FILING DATE: 1999-07-02  
: NUMBER OF SEQ ID NOS: 20  
: SOFTWARE: PatentIn Ver. 2.1  
: SEQ ID NO 10  
: LENGTH: 212  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-904-536-10  
Query Match 90.5%; Score 1124; DB 10; Length 212;  
Best Local Similarity 100.0%; Pred. No. 3e-91;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 25 GGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDELCGGLMRLVLAQRMWE 84  
Db 2 GGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDELCGGLMRLVLAQRMWE 61  
Qy 85 RLKTVAGSKMGGLELERNTEHFVTKCAFQPPPSCLRFVQTNISRLQETSEQLVALKRW 144  
Db 62 RLKTVAGSKMGGLELERNTEHFVTKCAFQPPPSCLRFVQTNISRLQETSEQLVALKRW 121

Qy 145 ITRONFSRCLCLOCPDSSSTLPMPSPRLATAPTAPQPELLLLLPVGLLLAAAC 204  
Db 122 ITRONFSRCLCLOCPDSSSTLPMPSPRLATAPTAPQPELLLLLPVGLLLAAAC 181  
Qy 205 LHMORTRRRTRPRGEGVPPVSPDILLVEH 235  
Db 182 LHMORTRRRTRPRGEGVPPVSPDILLVEH 212  
RESULT 6  
US-09-904-536-18  
: Sequence 18, Application US/09904536  
: Patent No. US20020111475A1  
: GENERAL INFORMATION:  
: APPLICANT: Graddis, Thomas J.  
: APPLICANT: McGrew, Jeffrey T.  
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
: FILE REFERENCE: 03260.0028  
: CURRENT APPLICATION NUMBER: US/09/904.536  
: CURRENT FILING DATE: 2001-07-16  
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
: PRIOR FILING DATE: 1999-07-02  
: NUMBER OF SEQ ID NOS: 20  
: SOFTWARE: PatentIn Ver. 2.1  
: SEQ ID NO 18  
: LENGTH: 209  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-904-536-18  
Query Match 89.7%; Score 1114; DB 10; Length 209;  
Best Local Similarity 100.0%; Pred. No. 2.2e-90;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDELCGGLMRLVLAQRMERL 86  
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDELCGGLMRLVLAQRMERL 60  
Qy 87 KTVAGSKMGGLELERNTEHFVTKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPWIT 146  
Db 61 KTVAGSKMGGLELERNTEHFVTKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPWIT 120  
Qy 147 RONFSRCLCLOCPDSSSTLPMPSPRLATAPTAPQPELLLLLPVGLLLAAACMLH 206  
Db 121 RONFSRCLCLOCPDSSSTLPMPSPRLATAPTAPQPELLLLLPVGLLLAAACMLH 180  
Qy 207 WORTRRRTRPRGEGVPPVSPDILLVEH 235  
Db 181 WORTRRRTRPRGEGVPPVSPDILLVEH 209  
RESULT 7  
US-09-904-536-9  
: Sequence 9, Application US/09904536  
: Patent No. US20020111475A1  
: GENERAL INFORMATION:  
: APPLICANT: Graddis, Thomas J.  
: APPLICANT: McGrew, Jeffrey T.  
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
: FILE REFERENCE: 03260.0028  
: CURRENT APPLICATION NUMBER: US/09/904.536  
: CURRENT FILING DATE: 2001-07-16  
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
: PRIOR FILING DATE: 1999-07-02  
: NUMBER OF SEQ ID NOS: 20  
: SOFTWARE: PatentIn Ver. 2.1  
: SEQ ID NO 9  
: LENGTH: 209  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-904-536-9

Query Match 89.4%: Score 1110; DB 10; Length 209;  
Best Local Similarity 99.5%; Pred. No. 5e-90;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAORMERL 86  
1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAORMERL 60

87 KTVAGSKMÖGILLERVNTIEHFVTKCAFQPPSCILRFVOTNISRLLOETSEQVLAALKPWIT 146  
61 KTVAGSKMÖGILLERVNTIEHFVTKCAFQPPSCILRFVOTNISRLLOETSEQVLAALKPWIT 120

147 RONSRCLELOCCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPPVGLLLAAACGLH 206  
121 RONSRCLELOCCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPPVGLLLAAACGLH 180

207 WQTRRRTPRPGEQVPVPSQDILLVEH 235  
181 WQTRRRTPRPGEQVPVPSQDILLVEH 209

RESULT 8  
US-09-904-536-12  
Sequence 12, Application US/09904536  
Patent No. US2002011475A1  
GENERAL INFORMATION:  
APPLICANT: Gradadis, Thomas J.  
APPLICANT: McGrew, Jeffrey T.  
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
FILE REFERENCE: 03260.0028  
CURRENT APPLICATION NUMBER: US/09/904,536  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
PRIOR FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentln Ver. 2.1  
LENGTH: 209  
SEQ ID NO 12  
TYPE: PR  
ORGANISM: Homo sapiens  
US-09-904-536-12

Query Match 89.4%: Score 1110; DB 10; Length 209;  
Best Local Similarity 99.5%; Pred. No. 5e-90;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAORMERL 86  
1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAORMERL 60

87 KTVAGSKMÖGILLERVNTIEHFVTKCAFQPPSCILRFVOTNISRLLOETSEQVLAALKPWIT 146  
61 KTVAGSKMÖGILLERVNTIEHFVTKCAFQPPSCILRFVOTNISRLLOETSEQVLAALKPWIT 120

147 RONSRCLELOCCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPPVGLLLAAACGLH 206  
121 RONSRCLELOCCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPPVGLLLAAACGLH 180

207 WQTRRRTPRPGEQVPVPSQDILLVEH 235  
181 WQTRRRTPRPGEQVPVPSQDILLVEH 209

RESULT 9  
US-09-904-536-14  
Sequence 14, Application US/09904536  
Patent No. US2002011475A1  
GENERAL INFORMATION:  
APPLICANT: Gradadis, Thomas J.  
APPLICANT: McGrew, Jeffrey T.  
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
FILE REFERENCE: 03260.0028  
CURRENT APPLICATION NUMBER: US/09/904,536

CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
PRIOR FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 14  
LENGTH: 209  
TYPE: PR  
ORGANISM: Homo sapiens  
US-09-904-536-14

Query Match 89.4%: Score 1110; DB 10; Length 209;  
Best Local Similarity 99.5%; Pred. No. 5e-90;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAORMERL 86  
1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAORMERL 60

87 KTVAGSKMÖGILLERVNTIEHFVTKCAFQPPSCILRFVOTNISRLLOETSEQVLAALKPWIT 146  
61 KTVAGSKMÖGILLERVNTIEHFVTKCAFQPPSCILRFVOTNISRLLOETSEQVLAALKPWIT 120

147 RONSRCLELOCCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPPVGLLLAAACGLH 206  
121 RONSRCLELOCCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPPVGLLLAAACGLH 180

207 WQTRRRTPRPGEQVPVPSQDILLVEH 235  
181 WQTRRRTPRPGEQVPVPSQDILLVEH 209

RESULT 10  
US-09-904-536-17  
Sequence 17, Application US/09904536  
Patent No. US2002011475A1  
GENERAL INFORMATION:  
APPLICANT: Gradadis, Thomas J.  
APPLICANT: McGrew, Jeffrey T.  
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
FILE REFERENCE: 03260.0028  
CURRENT APPLICATION NUMBER: US/09/904,536  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
PRIOR FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentln Ver. 2.1  
LENGTH: 209  
SEQ ID NO 17  
TYPE: PR  
ORGANISM: Homo sapiens  
US-09-904-536-17

Query Match 89.4%: Score 1110; DB 10; Length 209;  
Best Local Similarity 99.5%; Pred. No. 5e-90;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAORMERL 86  
1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAORMERL 60

87 KTVAGSKMÖGILLERVNTIEHFVTKCAFQPPSCILRFVOTNISRLLOETSEQVLAALKPWIT 146  
61 KTVAGSKMÖGILLERVNTIEHFVTKCAFQPPSCILRFVOTNISRLLOETSEQVLAALKPWIT 120

147 RONSRCLELOCCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPPVGLLLAAACGLH 206  
121 RONSRCLELOCCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPPVGLLLAAACGLH 180

207 WQTRRRTPRPGEQVPVPSQDILLVEH 235  
181 WQTRRRTPRPGEQVPVPSQDILLVEH 209

RESULT 11  
US-09-904-536-11  
Sequence 11, Application US/09904536  
Patent No. US2002011475A1  
GENERAL INFORMATION:  
APPLICANT: Graddis, Thomas J.  
APPLICANT: McGrew, Jeffrey T.  
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
FILE REFERENCE: 03260.0028  
CURRENT APPLICATION NUMBER: US/09/904,536  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
PRIOR FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 209  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-904-536-11

Query Match 89.2%; Score 1108; DB 10; Length 209;  
Best Local Similarity 99.5%; Pred. No. 7.4e-90;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 1 TODCSFOHSPISDFAVKIRELSDYLLQDYPTVASNLQDEELCGGLMRVLAQRMERL 86  
QY 87 KTVAGSKMOGLLEERVNTEIHFTVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146  
Db 61 KTVAGSKMOGLLEERVNTEIHFTVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120  
QY 147 RQNSRCLCLOCOPDSSSTLPWPMSRPLEATPTAPQPPDLLLLPVGLLLAAMCJH 206  
Db 121 RQNSRCLCLOCOPDSSSTLPWPMSRPLEATPTAPQPPDLLLLPVGLLLAAMCJH 180  
QY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235  
Db 181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209

RESULT 12  
US-09-904-536-15  
Sequence 15, Application US/09904536  
Patent No. US2002011475A1  
GENERAL INFORMATION:  
APPLICANT: Graddis, Thomas J.  
APPLICANT: McGrew, Jeffrey T.  
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
FILE REFERENCE: 03260.0028  
CURRENT APPLICATION NUMBER: US/09/904,536  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
PRIOR FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 209  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-904-536-15

Query Match 89.2%; Score 1108; DB 10; Length 209;  
Best Local Similarity 99.5%; Pred. No. 7.4e-90;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1 TODCSFOHSPISDFAVKIRELSDYLLQDYPTVASNLQDEELCGGLMRVLAQRMERL 86  
QY 27 TODCSFOHSPISDFAVKIRELSDYLLQDYPTVASNLQDEELCGGLMRVLAQRMERL 86  
Db 1 TODCSFOHSPISDFAVKIRELSDYLLQDYPTVASNLQDEELCGGLMRVLAQRMERL 60  
QY 87 KTVAGSKMOGLLEERVNTEIHFTVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146

Db 61 KTVAGSKMOGLLEERVNTEIHFTVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120  
QY 147 RQNSRCLCLOCOPDSSSTLPWPMSRPLEATPTAPQPPDLLLLPVGLLLAAMCJH 206  
Db 121 RQNSRCLCLOCOPDSSSTLPWPMSRPLEATPTAPQPPDLLLLPVGLLLAAMCJH 180  
QY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235  
Db 181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209

RESULT 13  
US-09-904-536-13  
Sequence 13, Application US/09904536  
Patent No. US2002011475A1  
GENERAL INFORMATION:  
APPLICANT: Graddis, Thomas J.  
APPLICANT: McGrew, Jeffrey T.  
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
FILE REFERENCE: 03260.0028  
CURRENT APPLICATION NUMBER: US/09/904,536  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
PRIOR FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 209  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-904-536-13

Query Match 89.1%; Score 1107; DB 10; Length 209;  
Best Local Similarity 99.5%; Pred. No. 9.1e-90;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 27 TODCSFOHSPISDFAVKIRELSDYLLQDYPTVASNLQDEELCGGLMRVLAQRMERL 86  
Db 1 TODCSFOHSPISDFAVKIRELSDYLLQDYPTVASNLQDEELCGGLMRVLAQRMERL 60  
QY 87 KTVAGSKMOGLLEERVNTEIHFTVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146  
Db 61 KTVAGSKMOGLLEERVNTEIHFTVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120  
QY 147 RQNSRCLCLOCOPDSSSTLPWPMSRPLEATPTAPQPPDLLLLPVGLLLAAMCJH 206  
Db 121 RQNSRCLCLOCOPDSSSTLPWPMSRPLEATPTAPQPPDLLLLPVGLLLAAMCJH 180  
QY 207 WQTRRRTPRPGEOVPPVPSPODLLLVEH 235  
Db 181 WQTRRRTPRPGEOVPPVPSPODLLLVEH 209

RESULT 14  
US-09-904-536-8  
Sequence 8, Application US/09904536  
Patent No. US2002011475A1  
GENERAL INFORMATION:  
APPLICANT: Graddis, Thomas J.  
APPLICANT: McGrew, Jeffrey T.  
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
FILE REFERENCE: 03260.0028  
CURRENT APPLICATION NUMBER: US/09/904,536  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100  
PRIOR FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 209  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-904-536-8

Query Match	89.0%;	Score 1106;	DB 10;	Length 209;
Best Local Similarity	99.5%;	Pred. No. 1.1e-89;		
Matches 208; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

0y 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLRVLAQRMERL 86  
 |||||  
 Db 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLRVLAQRMERL 60

Qy 87 KTVAGSKMGLLERVNTVEIHFTVKCAQPPSPCLRFVQVNIISRLQETSQDLALKPWIT 146  
 |||||  
 Db 61 KTVAGSKMGLLERVNTVEIHFTVKCAQPPSPCLRFVQVNIISRLQETSQDLALKPWIT 120

QY 147 RQNSRCLLEQCQPSSSTLPWPSPRLPEATAPAQPELLLLLVGLLLLAAMC<sub>LH</sub>.206  
|||||  
Db 121 RQNSRCLLEQCQPSSSTLPWPSPRLPEATAPAQPELLLLLVGLLLLAAMC<sub>LH</sub> 180

```

QY 207 WQTRRRRTPRGEGVPPVSPQDLLVEH 235
      |||||
Db 181 WQTRRRRTPRGEGVPPVSPQDLLVEH 209

```

### RESULT 15

US-09-904-536-16

Sequence 16, Application US/09904536

Patent No. US2002011475A1

; GENERAL INFORMATION:

APPLICANT: Graddis, Thomas J.

APPLICANT: McGrew, Jeffrey T

1. TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE

FILE REFERENCE: 03260.0028

CURRENT APPLICATION NUMBER: US/09/904,536

; CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 09/109,100

PRIOR FILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 20

```

SOFTWARE: PatentIn Ver. 2.1
;

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; SEQ ID NO 16

LENGTH: 209

TYPE: PRT

ORGANISM: *Homo sapiens*

ORGANISM: HU  
US-09-904-536-16

Query Match	88.6%;	Score 1100;	DB 10;	Length 209;
Best Local Similarity	99.5%;	Pred. No. 3.8e-89;		
Matches 208; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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0y 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLRLVLAQRMERL 86
|||||
Db 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLRLVLAQRMERL 60

```

QY 87 KTVAGSKMGLLERVNTIEIHVTKCAFPSPSCURFVOTNISRLLOETSEDLVALKPWIT 146  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 61 KTVAGSKMGLLERVNTIEIHFTVKCAFPSPSCURFVQNISRLLOETSELVALKPRIT 120

Oy 147 RQNSRCLFELQCQPSSSTLPWPSPRLVETAPTAQPPLLLLLLVGLLLAAACLH 206  
|||  
Dd 121 RQNSRCLFELQCQPSSSTLPWPSPRLVETAPTAQPPLLLLLLVGLLLAAACLH 180

```
QY 207 WQTRRRRTPRPGEQVPVPSPQDLLVEH 235
      |||||
Db 181 WQTRRRRTPRPGEQVPVPSPQDLLVEH 209
```

Search completed: May 27, 2003, 18:36:27  
Job time : 58 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:25:26 ; Search time 11 Seconds

(without alignments)  
886.085 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242

Sequence: 1 MTVLAPAMSPFTYLLLLLL.....RCEGVPPVPSQDLLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1242	100.0	235.1	FL3L_HUMAN
2	768	61.8	232.1	FL3L_MOUSE
3	92	7.4	661.1	AT12_VZVD
4	89.5	7.2	941.1	GBR2_HUMAN
5	89	7.2	387.1	SGCA_MESAU
6	89	7.2	793.1	S3A1_HUMAN
7	87.5	7.0	415.1	TNR3_MOUSE
8	87.5	7.0	479.1	MP1P_DROME
9	87	7.0	910.1	DDR1_RAT
10	87	7.0	911.1	DDR1_MOUSE
11	86.5	6.9	1394.1	CNG4_BOVIN
12	86	6.9	485.1	SSGP_VOICA
13	85	6.8	282.1	ATFS_HUMAN
14	85	6.8	366.1	FCGN_HUMAN
15	84.5	6.8	3726.1	ABFL_MOUSE
16	84	6.8	582.1	MNT_HUMAN
17	84	6.8	732.1	YF48_HUMAN
18	84	6.8	1234.1	NPHN_RAT
19	83.5	6.7	671.1	Z282_HUMAN
20	83	6.7	758.1	VKGC_HUMAN
21	82	6.6	2167.1	SHK1_RAT
22	81.5	6.6	488.1	MNT1_HUMAN
23	81.5	6.6	591.1	MNT_MOUSE
24	81.5	6.6	2124.1	Y192_HUMAN
25	81	6.5	283.1	ATFS_MOUSE
26	81	6.5	387.1	SGCA_MOUSE
27	81	6.5	428.1	EPIC_HUMAN
28	81	6.5	1248.1	DIAL_HUMAN
29	80.5	6.5	1402.1	IF4G_RABIT
30	80	6.4	397.1	CEPD_STRCL
31	80	6.4	940.1	GBR2_RAT
32	80	6.4	1174.1	KPC1_COCHOE
33	80	6.4	1794.1	YAV1_SCHPO

34	79	6.4	805.1	YGM6_YEAST	P53086 saccharomyc
35	78.5	6.3	251.1	HXB4_HUMAN	P17483 homo sapien
36	78.5	6.3	382.1	AVRB_RAT	P38445 rattus norv
37	78.5	6.3	387.1	SGCA_RABIT	Q28686 oryctolagus
38	78.5	6.3	913.1	DDR1_HUMAN	Q08343 h epithelia
39	78.5	6.3	1180.1	ATY1_HUMAN	Q9q11 homo sapien
40	78	6.3	205.1	CYSR_SYNY3	O55854 synechocyst
41	78	6.3	566.1	TS13_MOUSE	O01755 mus musculu
42	77.5	6.2	341.1	PLSX_VIRCH	Q9K94 vibrilo chol
43	77.5	6.2	1885.1	FAS2_CANAL	P43098 c fatty aci
44	77.5	6.2	2004.1	MOZ_HUMAN	Q92794 homo sapien
45	77	6.2	195.1	CORA_HPBVF	P29178 hepatitis b

## ALIGNMENTS

RESULT 1	FL3L_HUMAN	STANDARD:	PRT:	235 AA.
AC	P49771:			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3L).			
GN	FLT3LG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94195428; PubMed=8145851;			
RA	Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,			
RA	Bazan J.F., Kastelein N., Hudak S., Wagner J., Matson J., Luh J.,			
RA	Duda G., Martina N., Peterson D., Menon S., Shanaleit A.,			
RA	Muench M., Keilner G., Namikawa R., Rennick D., Roncarolo M.G.,			
RA	Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;			
RT	"Ligand for Flt3/Flk2 receptor tyrosine kinase regulates growth of			
RT	haematopoietic stem cells and is encoded by variant RNAs."			
RL	Nature 368:643-648(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94235842; PubMed=8180375;			
RA	Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,			
RA	Escobar S.S., Downey H., Splet R.R., Beckmann M.P., McKenna H.J.;			
RT	"Cloning of the human homologue of the murine Flt3 ligand: a growth			
RT	factor for early hematopoietic progenitor cells."			
RL	Blood 83:2795-2801(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.			
RX	MEDLINE=96032581; PubMed=7566977;			
RA	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,			
RT	Escobar S.;			
RT	"Structural analysis of human and murine Flt3 ligand genomic loci."			
RL	Oncogene 11:1165-1172(1995).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).			
RX	MEDLINE=20343011; PubMed=10881197;			
RA	Savvides S.N., Boone T., Karplus P.A.;			
RT	"Flt3 ligand structure and unexpected commonalities of helical			
RT	bundles and cystine knots."			
RL	Nat. Struct. Biol. 7:486-491(2000).			
CC	-I- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC			
CC	CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING			
CC	FACTORS AND INTERLEUKINS.			
CC	-I- SUBUNIT: Homodimer (isoform 2).			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);			
CC	secreted (isoform 2).			
CC	-I- ALTERNATIVE PRODUCTS: 2 isoforms: a 1/membrane-bound (shown here)			
CC	and 2/soluble; are produced by alternative splicing.			

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CC the European Bioinformatics Institute. There are no restrictions on its  
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DR EMBL: 004806; AAA1999.1; -  
DR EMBL: 003858; AAA19825.1; -  
DR EMBL: 029874; AAA90949.1; -  
DR EMBL: 029874; AAA90950.1; -  
DR PDB: 1ETE; 09-JUN-00  
DR Genew; HGNC:3766; FLT3LG.  
DR MIM: 600007; -  
DR InterPro: IPR004213; FLT3\_1lg.  
DR Pfam: PF02947; flt3\_1lg; 1.  
KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;  
KW 3D-structure.

FT SIGNAL 1 26 POTENTIAL.  
FT CHAIN 27 235 SL CYTOKINE.  
FT DOMAIN 27 184 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 185 205 POTENTIAL.  
FT DOMAIN 206 235 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 30 111  
FT DISULFID 70 153  
FT DISULFID 119 158  
FT CARBOHYD 126 126 N-LINKED (GLCNAC: .) (POTENTIAL).  
FT CARBOHYD 149 149 N-LINKED (GLCNAC: .) (POTENTIAL).  
FT VARSPLIC 161 178 DSSLPSPSPPLEATA -> VETVHFVSDGDLILNS  
(IN ISOFORM 2)  
FT VARSPLIC 179 235 MISSING (IN ISOFORM 2).  
FT VARSPLIC 72 72 G -> A (IN REF. 1).  
FT CONFLICT 72 72  
FT SEQUENCE 235 AA: 26416 MW: 7395BF63B4CECF CRC64;

Query Match 100.0%; Score 1242; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.1e-96;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MVTVLAPAMSPPTTYLLLLLLLLLSGLSGTQDCSFQHSPTSSDFAVKIRELSDYLLQDYPVTV 60  
DB 1 MVTVLAPAMSPPTTYLLLLLLLLLSGLSGTQDCSFQHSPTSSDFAVKIRELSDYLLQDYPVTV 60  
OY 61 AANLDEELCGGIMRLVLAQRMWRERLKYAGSMQGLLEVRNTEHFVYKCAQPPSPCL 120  
DB 61 AANLDEELCGGIMRLVLAQRMWRERLKYAGSMQGLLEVRNTEHFVYKCAQPPSPCL 120  
OY 121 REVQNTISRLQETSEQLVALKFWITRONFSRCLQLQCPDSSTLPPMSPRLEATAPT 180  
DB 121 REVQNTISRLQETSEQLVALKFWITRONFSRCLQLQCPDSSTLPPMSPRLEATAPT 180  
OY 181 AQPPLLLLLLPVGLLLAAAMCLMWQTRRRTPRPGGVPPVSPDILLVEH 235  
DB 181 AQPPLLLLLLPVGLLLAAAMCLMWQTRRRTPRPGGVPPVSPDILLVEH 235

## RESULT 2

FL3L\_MOUSE STANDARD; PRT; 232 AA.  
AC P49772; 064085;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE SL cytokine precursor (fms-related tyrosine kinase 3 ligand) (Flt3  
ligand) (Flt3l).  
GN FL3LG OR FL3L.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN 11  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94195428; PubMed=8145851;

RA Hannum C., Cuilpepper J., Campbell D., McClanahan T., Zurawski S.,  
RA Bazar J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,  
RA Duda G., Martina N., Peterson D., Menon S., Shafaroff A.,  
RA Muench M., Kelnar G., Namikawa R., Renick D., Roncarolo M.G.,  
RA Zlotnik A., Rosner O., Dubreuil P., Birnbaum D., Lee F.,  
RT "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of  
RT haematopoietic stem cells and is encoded by variant RNAs".  
RT Nature 368:643-648(1994).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN-SJL/J;  
RX MEDLINE=94084791; PubMed=7505204;  
RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,  
RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,  
RA Splett R.R., Fletcher F.A., Maraskovsky E., Farrar T.,  
RA Foxworth D., Williams D.E., Beckmann M.P.;  
RT "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase  
RT receptor: a proliferative factor for primitive hematopoietic cells".  
RL Cell 75:1157-1167(1993).  
RN (3)  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=96032581; PubMed=7566977;  
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,  
RA Escobar S.;  
RT "Structural analysis of human and murine flt3 ligand genomic loci".  
RL Oncogene 11:1165-1172(1995).  
RN (4)  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=95124710; PubMed=7824267;  
RA Lyman S.D., James L., Escobar S., Downey H., de Vries P.,  
RA Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,  
RA Cleveland L.S.;  
RT "Identification of soluble and membrane-bound isoforms of the murine  
RT flt3 ligand generated by alternative splicing of mRNAs".  
RL Oncogene 10:149-157(1995).  
RN (5)  
RP SEQUENCE FROM N.A.  
RA McClanahan T., Cuilpepper J., Campbell D., Wagner J.,  
RA Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J.,  
RA Mattei M.G., Rosnet O., Birnbaum D., Hannum C.;  
RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC  
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING  
CC FACTORS AND INTERLEUKINS.  
CC -1- SUBUNIT: Homodimer (soluble isoform) (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Two soluble  
CC isoforms are also produced by alternative splicing. One of which,  
CC isoform 3/E6, is biologically active, while the other, isoform  
CC 4/E6delta16, is inactive.  
CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2/5H, 3/E6  
CC and 4/E6delta16; are produced by alternative splicing.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).



FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 232 SL CYTOKINE.  
 FT DOMAIN 27 189 EXTRACELLULAR (POTENTIAL).  
 FT TRASMEM 190 210 POTENTIAL.  
 FT DOMAIN 211 232 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 31 112 BY SIMILARITY.  
 FT DISULFID 71 156 BY SIMILARITY.  
 FT DISULFID 120 161 BY SIMILARITY.  
 FT CARBOHYD 127 152 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 152 127 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT VARSPLIC 164 232 DSDTLPPSPALTEATELPEPRROLLELLELTLVL  
 FT VARSPLIC 164 232 LAAAGLRQARARREGLHPVLPSPH -> GNGPRAOH  
 FT VARSPLIC 164 232 HGATRLTATALTVCGLLPLVGTSHMEFLPYFLSLSE  
 FT VARSPLIC 164 232 LKMYLV (IN ISOFORM 2).  
 FT VARSPLIC 164 232 DSDTL -> GSHYAG (IN ISOFORM 3).  
 FT VARSPLIC 164 232 MISSING (IN ISOFORM 3).  
 FT VARSPLIC 164 232 VOCOP -> GLIMQARTLNKSSCLSVLSACIT (IN  
 FT VARSPLIC 164 232 ISOFORM 4).  
 FT CONFLICT 141 141 A -> G (IN REF. 1).  
 FT CONFLICT 198 198 MISSING (IN REF. 2).  
 SQ SEQUENCE 232 AA: 26141 MW: 3A3680D3CB69FBA6 CRC64:

Query Match 61.8%; Score 768; DB 1; Length 232;  
 Best Local Similarity 70.0%; Pred. No. 3.6e-57;  
 Matches 163; Conservative 17; Mismatches 43; Indels 10; Gaps 4;

OY 1 MYVLAPAWSP-TTYLLLLLSGLSTODCSFQSPISDFAVKIRELSDYLLQDYPVT 59  
 DB 1 MYVLAPAWSPNSLLLLLSLPCLTGTPDCYRSHSPISSEFKVKKRELTDLKIDYPT 60  
 OY 60 VASNLQDEELGGLWRLVLAQRMMERLKTAVGSKMOGLLEERVTEIHFVTKCAFPSPSC 119  
 DB 61 VAVNLQDEKCKKALMSLFLAQRWIEQLKTAVGSKMOTLEDVTEIHFVTSCEFOPLK 120  
 OY 120 LRVQCNISRLQETSEQLVALKPMYTR--QNFSCLELOCQDSDSTLPPMSPRPLEAT 177  
 DB 121 LRVQCNISRLQETSEQLVALKPMYTR--QNFSCLELOCQDSDSTLPPMSPRPLEAT 180  
 OY 178 APTAPQP---LTLLELLPVGLLLLAAMCLHMORTRRTPRPGEQVPVPSPP 227  
 DB 181 ELPEPRRQDLLLTLLELLPLTLVLLAAMCLHMORARRR---GELHPGVPLP 229

RESULT 3  
 ART2\_VZVD STANDARD: PRT: 661 AA.

AC P09264;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE Alpha trans-inducing factor 74 kDa protein.  
 GN 12.  
 OS Varicella-zoster virus (strain Dumas) (VZV).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_Taxid=10338;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86306657; PubMed=3018124;  
 RA Davison A.J., Scott J.E.;  
 RT "The complete DNA sequence of varicella-zoster virus.";  
 RL J. Gen. Virol. 67:1759-1816(1986).  
 CC -1- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT  
 CC ACTIVATION OF ALPHA GENES.  
 CC -----  
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DR EMBL: X04370; CAA27895.1; -.  
 DR PIR: C27342; TNBE12.  
 DR InterPro: IPR005051; Herpes\_UL46.  
 DR Pfam: PF03387; Herpes\_UL46; 1.  
 KW Transcription regulation; Trans-acting factor.  
 SQ SEQUENCE 661 AA: 74272 MW: C5CA77A16D365379 CRC64;

Query Match 7.4%; Score 92; DB 1; Length 661;  
 Best Local Similarity 26.6%; Pred. No. 2.7; Indels 36; Gaps 11;  
 Matches 61; Conservative 29; Mismatches 36;

OY 19 LLSGSLGTDGCS---FOHSPISDFAVKIRELSDYLLQDYPVTASNLQDEELCG- 71  
 DB 79 LTPSPVQSTERSHSLVGLGHHNNVPESLVSQMSNDVHGFQRMETIQCLDLDKLSGD 138  
 OY 72 GLMRLVLAQRMMERLKTAVGSKMOGLLEERVTEIHFVTKCAFP---PSCIRFV 123  
 DB 139 GLM-WVYENTYWOYLKTYTAEVPTSEKVKSKSTVLLFSSVNAKPISRHFKSKVI 197  
 OY 124 QTNISRLQETSEQLVALKPMYTRQNFSCLELOCQDSDSTLPPMSP-PLLEATAPAP 182  
 DB 198 NSDYRGICQELREALGAVQKYM---YFMR-----PDDPTNPSPTIRINQELTAATAT 247  
 OY 183 QPPLLLLLLPVGLLLLAAMCLHMORTRRTPRPGEQVPVPSPPDL 231  
 DB 248 GYGMWLFQDVID---ARVCRHLKQFRIRICPRASV---IPDDL 287

RESULT 4  
 GBR2\_HUMAN STANDARD: PRT: 941 AA.  
 ID GBR2\_HUMAN  
 AC G075899; G075974; G09UN9; G09UNR1; G09PIR2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Gamma-aminobutyric acid type B receptor, subunit 2 precursor (GABA-B  
 DE receptor 2) (GABA-B-R2) (Gb2) (GABABR2) (G protein-coupled receptor  
 DE 51) (GPR 51) (HG20).  
 GN GABBR2 OR GPR51.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN 11  
 RP SEQUENCE FROM N.A. (ISOFORM 2A).  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=99087321; PubMed=9872316;  
 RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,  
 RA Barnes A.A., Emson P., Ford S.M., Marshall F.H.;  
 RT "Heterodimerization is required for the formation of a functional  
 RT GABA(B) receptor.";  
 RL Nature 396:679-682(1998).  
 RN 12  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).  
 RC TISSUE=Brain;  
 RX MEDLINE=20193514; PubMed=10727622;  
 RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;  
 RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";  
 RL Brain Res. 860:41-52(2000).  
 RN 13  
 RP SEQUENCE FROM N.A. (ISOFORM 2A).  
 RA Liu M., Parker R., McCrear K., Watson J., Baker E., Sutherland G.,  
 RA Herzog H.;  
 RT "Cloning and characterization of a novel human GABA-B receptor subtype  
 RT with high affinity for GABA and low affinity for baclofen.";  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN 14  
 RP SEQUENCE FROM N.A. (ISOFORM 2A).  
 RC TISSUE=Hippocampus;  
 RA Borowsky B., Laz T., Gerald C.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN 15  
 RP SEQUENCE FROM N.A. (ISOFORM 2A).

RC TISSUE-Fetal brain;  
 RX MEDLINE=99189236; PubMed=10087195;  
 RA Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whitting P.,  
 RA Chateaufort A., Coulombe N., Kargman S., Caskey T., Evans J.F.,  
 RA O'Neill G.P., Liu Q.;  
 RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAR  
 RT receptors expressed predominantly in nervous tissues and mapped  
 RT proximal to the hereditary sensory neuropathy type 1 locus on  
 RT chromosome 9.";  
 RL Genomics 56:288-295(1999).  
 RN [6].  
 RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.  
 RC TISSUE-Brain;  
 RX MEDLINE=99263199; PubMed=10328880;  
 RA Martin S.C., Russek S.J., Farb D.H.;  
 RT "Molecular identification of the human GABAR2: cell surface  
 RT expression and coupling to adenylyl cyclase in the absence of  
 RT GABABR1.";  
 RL Mol. Cell. Neurosci. 13:180-191(1999).  
 RN [7].  
 RP R1A-R2 INTERACTION.  
 RX MEDLINE=99175124; PubMed=10075644;  
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,  
 RA Kargman S., Chateaufort A., Tsukamoto N., McDonald T., Whitting P.,  
 RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,  
 RA Bonner T.T., O'Neill G.P.;  
 RT "Identification of a GABAB receptor subunit, gb2, required for  
 RT functional GABAB receptor activity.";  
 RL J. Biol. Chem. 274:7607-7610(1999).  
 RN [8].  
 RP R1A-R2 INTERACTION.  
 RX MEDLINE=20237752; PubMed=10773016;  
 RA Sullivan R., Chateaufort A., Coulombe N., Kolakowski L.F. Jr.,  
 RA Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,  
 RA Abramowitz M., O'Neill G.P., Ng G.Y.K.;  
 RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))  
 RT receptors with truncated receptors and metabotropic glutamate  
 RT receptor 4 supports the GABA(B) heterodimer as the functional  
 RT receptor.";  
 RL J. Pharmacol. Exp. Ther. 293:460-467(2000).  
 CC -I- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS  
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,  
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,  
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES  
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE  
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC  
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING  
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC  
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT  
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE  
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN  
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM  
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND  
 CC ANTIINDOLEPTIN.  
 CC -I- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH  
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO  
 CC HAPPEN.  
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER  
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A  
 CC PREREQUISITE FOR MATURATION OF GABA-B-R1 TO THE  
 CC PLASMA MEMBRANE.  
 CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 2A (SHOWN HERE), 2B AND 2C. ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN  
 CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND  
 CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS  
 CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.  
 CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.  
 CC -I- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION  
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.  
 CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC GABA-B RECEPTOR SUBFAMILY.

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CC EMBL; AJ012188; CA099248.1; -  
 CC EMBL; AF056085; AAC63228.1; -  
 CC DR EMBL; AF095723; AAC63383.1; -  
 CC DR EMBL; AF095724; AAC63384.1; -  
 CC DR EMBL; AF095784; AAD30389.1; -  
 CC DR EMBL; AF074483; AAD03336.1; -  
 CC DR EMBL; AF069755; AAC93345.1; -  
 CC DR EMBL; AF099033; AAD45867.1; -  
 CC Genew; HGNC:4507; GPR51.  
 CC InterPro: IPR001828; ANF\_receptor.  
 CC InterPro: IPR000337; GPCR\_Mgr.  
 CC Pfam; PF00003; 7tm\_3; 1.  
 CC DR Pfam; PF01094; ANF\_receptor; 1.  
 CC DR PROSITE; PS00979; G\_PROTEIN\_REC\_F3\_1; FALSE\_NEG.  
 CC DR PROSITE; PS00980; G\_PROTEIN\_REC\_F3\_2; FALSE\_NEG.  
 CC DR PROSITE; PS00981; G\_PROTEIN\_REC\_F3\_3; FALSE\_NEG.  
 CC DR PROSITE; PS50259; G\_PROTEIN\_REC\_F3\_4; 1.  
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 CC KW Postsynaptic membrane; Coiled coil; Alternative splicing;  
 CC KW Polymorphism.  
 CC FT SIGNAL 1 41  
 CC FT CHAIN 42 941  
 CC FT  
 CC FT DOMAIN 42 483  
 CC FT TRANSMEM 484 504  
 CC FT DOMAIN 505 522  
 CC FT TRANSMEM 523 543  
 CC FT DOMAIN 544 551  
 CC FT TRANSMEM 552 572  
 CC FT DOMAIN 573 597  
 CC FT TRANSMEM 598 618  
 CC FT DOMAIN 619 654  
 CC FT TRANSMEM 655 675  
 CC FT DOMAIN 676 691  
 CC FT TRANSMEM 692 712  
 CC FT DOMAIN 713 720  
 CC FT TRANSMEM 721 741  
 CC FT DOMAIN 742 781  
 CC FT TRANSMEM 781 819  
 CC FT CARBOHYD 90 90  
 CC FT CARBOHYD 298 298  
 CC FT CARBOHYD 389 389  
 CC FT CARBOHYD 404 404  
 CC FT CARBOHYD 453 453  
 CC FT CARBOHYD 902 927  
 CC FT VARSPLIC 929 941  
 CC FT  
 CC FT VARIANT 628 628  
 CC FT  
 CC FT VARIANT 869 869  
 CC FT  
 CC FT CONFLICT 6 6  
 CC FT CONFLICT 12 12  
 CC FT CONFLICT 424 424  
 CC FT  
 CC FT SEQUENCE 941 AA; 105821 MW; 09E173DB0673C5D CRC64;  
 CC  
 CC Query Match 7.2%; Score 89.5; DB 1; Length 941;  
 CC Best Local Similarity 44.1%; Pred. No. 6.4;  
 CC Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;

OY 170 SPPPLEATAPTAQP-LLILLIPVGLLLAAMCLIMQRTTRRRPREGEVPPV 224  
 DB 3 SPPSGCPGPPPPPPPARLLILLIPVGLAAM-GW---ARGAPRRPPSSPL 56

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RESULT 5
SCA_MESAU
ID SCA_MESAU STANDARD: PRT: 387 AA.
AC 064255;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-sarcoglycan precursor (Alpha-5G) (Adhaliin) (50 kda dystrophin-
associated glycoprotein) (50DAG).
GN SCA.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-Syrian; TISSUE=Heart muscle;
RX MEDLINE=98054328; PubMed=9391120;
RA Sakamoto A., Ono K., Abe M., Jasmin G., Ekl T., Murakami Y.,
RA Masaki T., Toyooka T., Hanaoka F.;
RT "Both hypertrophic and dilated cardiomyopathies are caused by mutation
of the same gene, delta-sarcoglycan, in hamster: an animal model of
disrupted dystrophin-associated glycoprotein complex.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN-F1B; TISSUE=Skeletal muscle;
RX MEDLINE=95278335; PubMed=7758576;
RA Roberts S.L., Campbell K.P.;
RT "Adhaliin mRNA and cDNA sequence are normal in the cardiomyopathic
hamster";
RT FEBS Lett. 364:245-249(1995).
CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX. A SUBCOMPLEX OF
F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Sarcolemmal
(potential).
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND
HEART MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.
CC
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CC
DR EMBL: D83651; BAA12025.1;
DR EMBL: U21677; AAA81645.1;
KW Cytoskeleton; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 387 ALPHA-SARCOGLYCAN.
FT DOMAIN 24 290 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 291 311 POTENTIAL.
FT DOMAIN 312 387 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 209 335 CIS-RICH.
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 387 AA; 43326 MW; D8599C0FAF646C3F CRC64;

Query Match 7.28; Score 89; DB 1; Length 387;
Best Local Similarity 23.48; Pred. No. 2.6;
Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

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Db 162 GGLMELGELQILNITSALDRGRVPLPIEGRKEGVYIKVGSATPSTCLKNVSPDSYAR 221
Qy 111 CAFOPPP---SC-----LRPVQTNISRLDQETSQVYALKWITRONFSRLQCCPD 161
Db 222 CAQGQRPPLSCDYLAPHRVDMCNVSLVDSVPEPLD-----EVPQPD 266
Qy 162 SSTLRPPSPRLPEAT-----APTAPQPLLLLLLPGVLLLAAMC----- 204
Db 267 GLENDPFPCCPTTEATGDLADALVTLLVPLVALLL---TLLAYIMCRRQGLKRD 323
Qy 205 -----LHMORTRRRTPRP-----GEQVPP-VPSPQ-DLL 231
Db 324 MATSDIQVNHCTINGNTEELRQMAARREVPRLSTLPMFNVTGRLPRPVDASQVPLI 383
Qy 232 LVEH 235
Db 384 LDQH 387

RESULT 6
SCA1_HUMAN
ID SCA1_HUMAN STANDARD: PRT: 793 AA.
AC Q15459;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Splicing factor 3 subunit 1 (Spliceosome associated protein 114) (SAP
114) (SF3A120).
GN SF3A1 OR SAP114.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE=96079958; PubMed=7489498;
RA Kremer A., Mulhauser F., Weisig C., Groning K., Bilbe G.;
RT "Mammalian splicing factor SF3A120 represents a new member of the
RT SUPR family of proteins and is homologous to the essential splicing
factor PRP21p of Saccharomyces cerevisiae.";
RT RNA 1:260-272(1995).
RN 12;
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burhill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Cleeg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dharmi P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French K., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Pamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Matryn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMuray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilmimg L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Aoki N., Mitsuyma S.,
RA Shintani A., Shibuya K., Yoshizaki Y., Asakawa S., Kudoh J.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorfman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Lon P., Malaj P., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Williamson D., Wu H., Yao Z.,

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RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Mux P.,  
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
 RA Cordes M., Du Z., Fulton L., Goele D., Graves T., Hawkins J.,  
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozerik P., Rolfing T.,  
 RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,  
 RA Korfi I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,  
 RA Emanuel B.S., Shaikh T., Kuranishi H., Saitta S., Budarf M.L.,  
 RA Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,  
 RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,  
 RA Serousi E., Franssion I., Tapia I., Bruder C.E., O'Brien K.P.,  
 RA Wilkinson P., Bodetrich A., Hartman K., Hu X., Khan A.S., Lane L.,  
 RA Tilahun Y., Wright H.;  
 RA "The DNA sequence of human chromosome 22.";  
 RL Nature 402:489-495(1999).  
 RN [3]  
 RP CHARACTERIZATION OF THE SPLICEOSOME.  
 RX MEDLINE:20337962; PubMed:10882114;  
 RA Das R., Zhou Z., Reed R.;  
 RT "Functional association of U2 snRNP with the ATP-independent  
 RT spliceosomal complex E.";  
 RL Mol. Cell 5:779-787(2000).  
 CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'  
 CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE  
 CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT  
 CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS  
 CC ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE  
 CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.  
 CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF  
 CC THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP14. SF3A  
 CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO  
 CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).  
 CC INTERACTS WITH SF3A3.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.  
 CC -1- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.  
 CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.  
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 CC -----  
 DR EMBL: X85237; CA939494.1; -;  
 DR EMBL: AC004997; AAC23435.1; -;  
 DR HSSP: Q15843; INDD.  
 DR GeneW: HGNC:10765; SF3A1.  
 DR MIM: 605595; -;  
 DR InterPro: IPR000061; Surp.  
 DR InterPro: IPR000626; Ubiquitin.  
 DR Pfam: PF00240; ubiquitin.1.  
 DR SMART: SM00213; UBO; 1.  
 DR PROSITE: PS50053; UBQUITIN\_2; 1.  
 KM SPLICEOSOME: mRNA processing; mRNA splicing; Nuclear protein; Repeat.  
 FT REPEAT 52 94 SURP MOTIF 1.  
 FT REPEAT 166 208 SURP MOTIF 2.  
 FT DOMAIN 707 793 UBQUITIN-LIKE.  
 FT DOMAIN 10 16 POLY-PRO.  
 FT DOMAIN 118 122 POLY-GLN.  
 FT DOMAIN 260 267 POLY-GLU.  
 FT DOMAIN 369 372 POLY-PRO.  
 FT DOMAIN 357 560 POLY-PRO.  
 FT DOMAIN 672 675 POLY-PRO.  
 SQ SEQUENCE 793 AA; 88886 MW; 7259F1EC4577305C CRC64;  
 Query Match 7.2%; Score 89; DB 1; Length 793;  
 Best Local Similarity 22.3%; Pired. No. 5.8;  
 Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

DB 401 LPPAPADEYL-----SPITGE---KI-----PASK 424  
 QY 64 LODELGGGLMRVLAORWME-RLKTV-----AGSKOGILLERVNTETHF 107  
 DB 425 MOEIMRG-----LLDRWLEQRDRSIREKOSDDEVAPGLDISSIKOLAE-RTIFG 478  
 QY 108 VTKCA-----FQPPPSCLRF-----VQTNISRLQETSEGLVLRPWI 145  
 DB 479 VEEFAIGKKIGEEELQKPEEKVTWDGSHGSMARQQAQANIT--LOEILEAIHKRAGLV 536  
 QY 146 -----TRQNF--SRLELQCP-----DSSLTP-----PWSRPLEAT-----APT 180  
 DB 537 PEDTKERIGPSKPELEIPQPPSSATNIPSSAPITTSVPRPTMPPVATTVSAVPV 596  
 QY 181 APQPLLLLLLPVGLLLLAAMCLHWRTR-----RTRPRGEQVP--VPSP 227  
 DB 597 MPRPMSVNLPPGVSVAIAPRPIIHAIRINVMPSAPRPIAPRPPMIVPAFAVPAP 656  
 RESULT 7  
 TNR3 MOUSE STANDARD; PRT; 415 AA.  
 ID TNR3 MOUSE  
 AC P50284;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 3 precursor  
 DE (lymphotoxin-beta receptor).  
 GN LTRB OR TNFRSF3 OR TNFR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:CVB; TISSUE:Lung;  
 RX MEDLINE=96072804; PubMed=7594541;  
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
 RA Browning J.L., Ware C.F.;  
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
 RT and expression.";  
 RL J. Immunol. 155:5280-5286(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96163885; PubMed=8586432;  
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,  
 RA Honjo T.;  
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
 RT sequence trap and chromosomal mapping.";  
 RL Genomics 30:312-319(1995).  
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
 CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3  
 CC and TRAF5. May play a role in the development of lymphoid organs  
 CC (By similarity).  
 CC -1- SUBUNIT: self-associates (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -----  
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 CC -----  
 DR EMBL: U29173; AAA68964.1; -;  
 DR EMBL: L38423; AAB00846.1; -;  
 DR EMBL: U30798; AAA81334.1; -;  
 DR HSSP: O14763; IDOG.  
 DR MCD: MGI:104875; Ltbr.  
 DR InterPro: IPR001368; TNFR\_C6.

DR Pfam: PF00020; TNFR\_c6; 3.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR\_3.  
 DR PROSITE: PS00552; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS00500; TNFR\_NGFR\_2; 3.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 415  
 FT DOMAIN 31 223  
 FT TRANSMEM 224 244  
 FT DOMAIN 245 415  
 FT REPEAT 42 81  
 FT REPEAT 82 124  
 FT REPEAT 125 170  
 FT REPEAT 171 213  
 FT DISULFID 43 58  
 FT DISULFID 59 72  
 FT DISULFID 62 80  
 FT DISULFID 83 98  
 FT DISULFID 101 116  
 FT DISULFID 104 124  
 FT DISULFID 126 132  
 FT DISULFID 139 150  
 FT DISULFID 142 169  
 FT DISULFID 172 187  
 FT CARBOHYD 40 40  
 FT CARBOHYD 179 179  
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEFF601 CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 415;  
 Best Local Similarity 24.4%; Pred. No. 3.7;  
 Matches 39; Conservative 20; Mismatches 52; Indels 49; Gaps 8;

QY 110 KCAFPQPPSL-----RFV-----QTNISRLQETSEQLVAKPMITRONFS 151  
 DB 123 ECHQCPQMSGVYDNECVHCEEBRLVACQPTAEVDEIDNDVNCVPCPKGHQNTSS 182  
 QY 152 RCELEACQPSSTLPWMSRPLEATAP-----TAPQPPULLLLLPVGLL--- 198  
 DB 183 P--RAKQPIHRC-----ELQGLEVAAPGYSYSTPTICKNPPKAMLLAILLSLVFL 235  
 QY 199 ----LAAWCLHWQTR-----RRPRPGEQVPPVPSQ 228  
 DB 236 FTVLACQAMRHPSLCKRLKLTGLKRHPE-GEESPCCAPR 274

RESULT 8  
 MPID\_DROME STANDARD; PRT; 479 AA.  
 ID MPID\_DROME STANDARD; PRT; 479 AA.  
 AC P20483; Q9VAL9;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 15-phase inducer phosphatase (EC 3.1.3.48) (String protein) (Cdc25-1-like protein).  
 GN STG OR CDC25 OR CG1395.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89195217; PubMed=2702688;  
 RA Edgar B.A., O'Farrell P.H.;  
 RT "Genetic control of cell division patterns in the Drosophila embryo.";  
 RL Cell 57:177-187(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91006056; PubMed=2120044;  
 RA Jimenez J., Alphey L., Nurse P., Glover D.M.;  
 RT "Complementation of fission yeast cdc2ts and cdc25ts mutants

RT identifies two cell cycle genes from Drosophila: a cdc2 homologue and  
 RT string";  
 RL EMBO J. 9:3565-3571(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,  
 RA Beeson K.Y., Bens P.V., Berman B.P., Brothier P., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brothier P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mikhlov G., Misha N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskens D.R., Paclet J.M.,  
 RA Palazzolo M., Plutman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSE-DEPENDENT INDUCER IN  
 CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR  
 CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE  
 CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SIMILARITY: BELONGS TO THE MPI PHOSPHATASE FAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 RHODANEST DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: M24909; AAA28916.1; -;  
 DR EMBL: X57495; CAA40732.1; -;  
 DR EMBL: AE003768; AAF56885.1; -;  
 DR PIR: A32290; A32290.  
 DR PIR: S12008; S12008.  
 DR HSP: P30304; IC25.  
 DR FLYBASE: FBgn0003525; stg  
 DR InterPro: IPR000751; MPI\_phosphatase.  
 DR InterPro: IPR001763; Rhodanese-1like.  
 DR Pfam: PF00581; Rhodanese-1.  
 DR PRINTS: PR00716; MPIPHPTASE.



DE (DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase  
DE MPK-6).  
DE DDRI OR EDDRI OR CAK OR MPK6.  
OS Mus musculus (mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC STRAIN=C57BL/6;  
RX MEDLINE=96204002; PubMed=8622863;  
RA Perez J.L., Jing S.Q., Wong T.W.;  
RT "Identification of two isoforms of the Cak receptor kinase that are  
RT coexpressed in breast tumor cell lines.";  
RL Oncogene 12:1469-1477(1996).  
RN [2]  
RP SEQUENCE OF 766-822 FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Embryonic brain;  
RA MEDLINE=93096484; PubMed=1281307;  
RA Giliardi-Hebensstreit P., Nieto M.A., Frain M., Mattei M.-G.,  
RA Chestier A., Wilkinson D.G., Charnay P.;  
RT "An Eph-related receptor protein tyrosine kinase gene segmentally  
RT expressed in the developing mouse hindbrain.";  
RL Oncogene 7:2499-2506(1992).  
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND  
CC RECOGNITION (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK II;  
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE  
CC ABSENCE OF A 37 RESIDUES SEGMENT.  
CC -1- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN  
CC DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS  
CC EPITHELIAL CELLS.  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN  
CC RECEPTOR SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.  
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CC -----  
DR EMBL: L57509; AAB05209.1; -;  
DR EMBL: X57240; CA440516.1; -;  
DR PIR: S30502; S30502.  
DR HSSP: P00523; 2PTRK.  
DR MGD: MGI:99216; Ddr1.  
DR InterPro: IPR000719; Euk.pkinase.  
DR InterPro: IPR000421; FA58.C.  
DR InterPro: IPR002011; RTKinaseIT.  
DR InterPro: IPR001245; Tyr.pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR Pfam: PF00754; F5\_F8\_TypeC; 1.  
DR Prodom: PD000001; Euk.pkinase; 1.  
DR SMART: SM00231; FA58C; 1.  
DR SMART: SM00219; TyrKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_LI; 1.  
DR PROSITE: PS01285; FA58C\_1; 1.  
DR PROSITE: PS01286; FA58C\_2; 1.  
KW Transferase: Tyrosine-protein kinase; Glycoprotein; Signal;  
KW Phosphorylation; Transmembrane; Receptor; ATP-binding;  
KW Alternative splicing.  
FT CHAIN 1 19 POTENTIAL.  
FT SIGNAL 20 414 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.  
FT DOMAIN 20 414 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 415 441 POTENTIAL.  
FT DOMAIN 442 911 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 32 186 F5/8 TYPE C (PHOSPHOLIPID-BINDING,  
FT POTENTIAL).  
FT DOMAIN 379 413 GLY/PRO-RICH.  
FT DOMAIN 474 599 GLY/PRO-RICH.  
FT DOMAIN 608 902 PROTEIN KINASE.  
FT NP\_BIND 614 622 ATP (BY SIMILARITY).  
FT BINDING 653 653 ATP (BY SIMILARITY).  
FT ACT\_SITE 764 764 BY SIMILARITY.  
FT DISULFID 32 186 BY SIMILARITY.  
FT MOD\_RES 511 511 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT MOD\_RES 790 790 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT MOD\_RES 794 794 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT MOD\_RES 795 795 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 262 372 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 503 539 MISSING (IN ISOFORM CAK II).  
SQ SEQUENCE 911 AA; 101160 MW; DB87FE03DD079510 CRC64;  
  
Query Match 7.0%; Score 87; DB 1; Length 911;  
Best Local Similarity 24.5%; Pred. No. 10;  
Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;  
  
QY 143 PWITRONSRLLELQCCDSSSTLP-PW---SPRLXETA---PTAQP----- 184  
Db 357 PWLLESEISFISDV-VNDSSTFPAPWPPGPPPTNFSLELEPGQPVAKAGSPTA 415  
QY 185 -----PULLLLLPVGLLLAAMCLHMOR---TFRR-----T 214  
Db 416 ILICGLVAIIILLILLIIMLM-----WRHWRRLSKARRVLEELTVHLSVPGDTILIN 471  
QY 215 PRGEQVPP-----VSPQDLL 232  
Db 472 NRPGRPEPPYQEPNRPCTPPHSAFCVNGSALL 506  
  
RESULT 11  
CNG4\_BOVIN STANDARD; PRT; 1394 AA.  
AC Q28181; Q28082; Q03861;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 240 kDa protein of rod photoreceptor CNG-channel [contains: Glutamic  
DE acid-rich protein (GARP): Cyclic-nucleotide-gated cation channel 4  
DE (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel  
DE modulatory subunit)].  
GN CNGB1 OR CNGC4.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
ON NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=96009859; PubMed=7546742.  
RA Goerz S., Colville C., Mueller F., Dose A., Godde M., Molday L.,  
RA Kaupp U.B., Molday R.S.;  
RT "A 240 kDa protein represents the complete beta subunit of the cyclic  
RT nucleotide-gated channel from rod photoreceptor.";  
RL Neuron 15:627-636(1995).  
RN [2]  
RP SEQUENCE OF 454-1394 FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=96198098; PubMed=8626431;  
RA Biel M., Zong X., Ludwig A., Sauter A., Hofmann F.;  
RT "Molecular cloning and expression of the modulatory subunit of the  
RT cyclic nucleotide-gated cation channel.";  
RL J. Biol. Chem. 271:6349-6355(1996).



[3]  
 RN SEQUENCE OF 1-590 FROM N.A.  
 RP TISSUE-RETIKA;  
 RA Suimico Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;  
 RL Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBMITT: FORMS FUNCTIONAL HETEROLOGICOMERIC CHANNELS WITH CNG3.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: CNG4C (SHOWN HERE), CNG4D  
 CC AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR  
 CC THE MOST FREQUENT FORM (CNG4D:CNG4C:CNG4E = 20:2:1) IN TESTIS.  
 CC -1- TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X89626; CAA61769.1; -;  
 DR EMBL: X94707; CAA64367.1; -;  
 DR EMBL: M61185; AAA30536.1; -;  
 DR InterPro: IPR000636; M-channel\_nlg  
 DR InterPro: IPR000595; CNMP\_binding.  
 DR Pfam: PF00027; CNMP\_binding; 1.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR SMART: SM00100; CNMP; 1.  
 DR PROSITE: PS00888; CNMP\_BINDING\_1; 1.  
 DR PROSITE: PS00889; CNMP\_BINDING\_2; 1.  
 DR PROSITE: PS50042; CNMP\_BINDING\_3; 1.  
 DR PROSITE: PS50042; CNMP\_BINDING\_3; 1.  
 DR Ionic channel; Ion transport; CNMP-binding; Transmembrane;  
 KW Multigene family; Alternative splicing.  
 FT CHAIN 1 590  
 FT DOMAIN 1 767  
 FT TRANSMEM 768 786  
 FT DOMAIN 787 800  
 FT TRANSMEM 801 819  
 FT DOMAIN 821 844  
 FT TRANSMEM 845 864  
 FT DOMAIN 865 901  
 FT TRANSMEM 902 924  
 FT DOMAIN 925 968  
 FT TRANSMEM 969 988  
 FT DOMAIN 1073 1093  
 FT TRANSMEM 1094 1394  
 FT NP\_BIND 1081 1219  
 FT BINDING 1141 1141  
 FT BINDING 1153 1153  
 FT CARBOHYD 1067 1067  
 FT VARSPPLIC 515 532  
 FT VARSPPLIC 522 530  
 FT CONFLICT 341 341  
 FT CONFLICT 454 465  
 FT CONFLICT 482 482  
 FT CONFLICT 499 499  
 FT CONFLICT 572 590  
 FT CONFLICT 1283 1283  
 FT CONFLICT 1289 1289  
 FT CONFLICT 1336 1336  
 FT CONFLICT 1338 1338  
 SO SEQUENCE 1394 AA; 155064 MW; EE6DA559BE3744A7 CRC64;  
 Query Match 7.0%; Score 86.5; DB 1; Length 1394;  
 Best Local Similarity 24.6%; Pred. No. 18;  
 Matches 35; Conservative 13; Mismatches 53; Indels 41; Gaps 5;  
 QY 115 PPSGLRFVQNTISRL-----QTSQVLAALKWITRONTSRL 154

DB 163 PGWLLRWEQNLEKMLPPPKISEGWRDEPDALGPEPPGALIKPMLQAQ----- 216  
 QY 155 ELQCCPDSSTLPWPSPRLPEATAPAPOPPLLLLPVGLLLLAAMCLHMQRTRRT 214  
 DB 217 -----ESSSLRPGGPEEBEERIP-EPOPTIOASSLPPODSARLAMIILH--RIEMAL 267  
 QY 215 PRP-----GEQVPPVSPDOL 230  
 DB 268 PQVIRKGGEQESDAPVCDV 289  
 RESULT 12  
 SSGP\_VOLCA STANDARD; PRT; 485 AA.  
 AC P21997;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Sulfated surface glycoprotein 185 (SSG 185).  
 OS Volvox carterii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Volvocaceae; Volvox.  
 OX NCBI\_TaxID=3067;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=F. Nagariensis / HK10;  
 RA MEDLINE=90094551; PubMed=2689458;  
 RX Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;  
 RT "The extracellular matrix of Volvox carterii: molecular structure of  
 RT the cellular compartment."  
 RL J. Cell Biol. 109:3493-3501(1989).  
 CC -1- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS  
 CC INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A  
 CC DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE  
 CC MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C32 STRUCTURE). THE  
 CC COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS  
 CC RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.  
 CC -1- PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF  
 CC HYDROXYPROLINE RESIDUES.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X51616; CAA35953.1; -;  
 DR PIR: A33647; A33647.  
 KW Glycoprotein; Sulfation; Hydroxylation.  
 FT DOMAIN 228 340  
 FT DOMAIN 260 295  
 FT POLY-PRO.  
 SO SEQUENCE 485 AA; 50436 MW; A52216400A031421 CRC64;  
 Query Match 6.9%; Score 86; DB 1; Length 485;  
 Best Local Similarity 29.2%; Pred. No. 5.9;  
 Matches 21; Conservative 3; Mismatches 22; Indels 26; Gaps 1;  
 QY 160 PDSSTLPWPSPRLPEATAPAPOPPLLLLPVGLLLLAAMCLHMQRTRRRPRPGE 219  
 DB 275 PPSPPPPPPPPPPPPPPPPPPSP-----RKPPSPSP 308  
 QY 220 QVPPVSPDOLL 231  
 DB 309 PVPPPPSPSVL 320  
 RESULT 13  
 ATFS\_HUMAN STANDARD; PRT; 282 AA.  
 AC Q9Y2D1; Q9UN03;



DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cyclic-AMP-dependent transcription factor ATF-5 (Activating  
 DE transcription factor 5) (transcription factor ATF5).  
 GN ATF5 OR ATF5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=20558615; PubMed=11087824;  
 RA White J.H., McIlhinney R.A.J., Wise A., Ciruela F., Chan W.Y.,  
 RA Emson P.C., Billington A., Marshall F.H.;  
 RT "The GABA<sub>B</sub> receptor interacts directly with the related transcription  
 RT factors CREB2 and ATF5.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:13967-13972(2000).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RA Kohroki J., Tanaka K.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE OF 161-282 FROM N.A.  
 RX MEDLINE=99303793; PubMed=10373550;  
 RA Patl D., Meistrich M.L., Pilon S.E.;  
 RT "Human Cdc34 and Rad6 ubiquitin-conjugating enzymes target repressors  
 RT of cyclic AMP-induced transcription for proteolysis.";  
 RL Mol. Cell. Biol. 19:5001-5013(1999).  
 CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)  
 CC (CONSENSUS: 5'(GTGACGT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN MANY  
 CC VIRAL AND CELLULAR PROMOTERS.  
 CC -1- SUBUNIT: BINDS DNA AS A DIMER (POTENTIAL). INTERACTS WITH GABA<sub>B</sub>  
 CC RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AF305687; AAC22558.1; -  
 CC EMBL: AB021663; BA78477.2; -  
 CC EMBL: AF101388; AAD28370.1; -  
 CC TRANSFAC: T04877; -  
 CC DR Genew; HGNC:790; ATF5.  
 CC DR MIM; 606398; -  
 CC DR InterPro: IPR004827; TF\_BZIP.  
 CC DR Pfam; PF00170; bZIP.1.  
 CC DR SMART; SM00338; BRLZ.1.  
 CC DR SMART; PS00036; BZIP\_BASIC.1.  
 CC DR Transcription regulation; DNA-binding; Activator; Nuclear protein;  
 CC KM Multigene family.  
 CC FT DOMAIN 123 139 POLY-PRO.  
 CC FT DOMAIN 186 194 POLY-PRO.  
 CC FT DOMAIN 210 230 BASIC MOTIF.  
 CC FT DOMAIN 236 250 LEUCINE-ZIPPER (PROBABLE).  
 CC FT CONFLICT 161 163 LLA -> RHE (IN REF. 3).  
 CC SEQUENCE 282 AA; 30674 MW; DDB2P907CA0215A0 CRC64;  
 SO  
 Query Match 6.88; Score 85; DB 1; Length 282;  
 Best Local Similarity 29.98; Pred. No. 3.9;  
 Matches 38; Conservative 7; Mismatches 38; Indels 44; Gaps 6;  
 Oy 144 WIT-RONSRCLTQCPDSTLPPWSPRP--LEATA-----178  
 Db 66 WMTRRVDTALLPLPEPPPTLQPP--SPYPPDLKAAVSLIKKELEQMEDFFLAPLPP 124  
 Oy 179 ---PTAPQPLLLLLLPVGL-----LLIAAWCLH--MORTRRRTPRPGQ 220

Db 125 PSPPLPLPPLPAPASPLSLPSRFDLPQPVYLDLIDLAIYCRNAGEVGMPLPPQ 184  
 Oy 221 VPPVPSP 227  
 Db 185 QPPPPSP 191  
 RESULT 14  
 FCGR1\_RAT  
 ID FCGR1\_RAT STANDARD; PRT; 366 AA.  
 AC P13599;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Igg receptor FCGR1 large subunit P51 precursor (FCRN) (Neonatal FC  
 DE receptor) (IGG FC fragment receptor transporter, alpha chain).  
 GN FCGR1 OR FCGR1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=Mistar;  
 RX MEDLINE=89097257; PubMed=2911353;  
 RA Simister N.E., Mostov K.E.;  
 RT "An Fc receptor structurally related to MHC class I antigens.";  
 RL Nature 337:184-187(1989).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Epithelium;  
 RX MEDLINE=90315866; PubMed=2534798;  
 RA Simister N.E., Mostov K.E.;  
 RT "Cloning and expression of the neonatal rat intestinal Fc receptor, a  
 RT major histocompatibility complex class I antigen homolog.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).  
 RN [3]  
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=90594982; PubMed=7969498;  
 RA Burneister W.P., Huber A.H., Bjorkman P.J.;  
 RT "Crystal structure of the complex of rat neonatal Fc receptor with  
 RT Fc.";  
 RL Nature 372:379-383(1994).  
 RN [4]  
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=98154319; PubMed=9493268;  
 RA Vaughn D.E., Bjorkman P.J.;  
 RT "Structural basis of pH-dependent antibody binding by the neonatal Fc  
 RT receptor.";  
 RL Structure 6:63-73(1998).  
 CC -1- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS  
 CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS  
 CC NEONATAL ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS  
 CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE  
 CC RESULTANT FCRN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE  
 CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCRN INTO BLOOD OR  
 CC TISSUE FLUIDS (BY SIMILARITY).  
 CC -1- SUBUNIT: FCRN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH  
 CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-  
 CC LIKE HETERODIMER.  
 CC -1- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM SUPERMAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC -----  
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 CC -----

DR EMBL: X14323; CAA32503.1; -  
 DR EMBL: M35495; AAA41611.1; -  
 DR PIR: S02117; S02117.  
 DR PIR: A37374; A37374.  
 DR PDB: 1ERT; 1A-FEB-95.  
 DR PDB: 3FRU; 10-JUN-98.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR01039; MHC\_I.  
 DR Pfam: PF00047; Ig; 1.  
 DR Pfam: PF00129; MHC\_I; 1.  
 DR ProDom: PD000050; MHC\_I; 1.  
 DR SMART; SM00407; Igcl; 1.  
 DR PROSITE; PS00290; Ig\_MHC; 1.  
 DR IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 366 ICG RECEPTOR FCAN LARGE SUBUNIT P51.  
 FT DOMAIN 23 111 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 112 201 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 202 291 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 292 298 CONNECTING PEPTIDE.  
 FT TRANSMEM 299 322 POTENTIAL.  
 FT DOMAIN 323 366 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 120 183 BY SIMILARITY.  
 FT DISULFID 222 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 366 AA; 40168 MW; 8ABBF2873A698B85 CRC64;

Query Match 6.8%; Score 85; DB 1; Length 366;  
 Best Local Similarity 22.2%; Pred. No. 5.2;  
 Matches 51; Conservative 21; Mismatches 66; Indels 92; Gaps 11;

QY 46 RELSDVLLDYPYTVASNLQDELGLMPLVLAQRMME---RLKTVAGSKMOGLLEEV 101  
 DB 173 RESEFLITSCP-----ERLLGLHLEGRQNLKEMKEPPSMRLKARPNGSSSVL--- 220  
 QY 102 NNEIHVTSCA---FQPPSCSLRFVQTNISRLQETSEQLVALKPMITRONFSRC----- 153  
 DB 221 -----TCAASFYFPELKFRLNGLA-----SGSGNCSTGPN 253  
 QY 154 -----LEL-----OCQDPSSTLPWPSPRPLEATAPAPQPLLLLLLPVG 195  
 DB 254 GDGSFHWLSLLEVKRGDEHHYQCQVEHGLAQPLT---VDLDSPARSSVYVCGIIL---G 307  
 QY 196 LLLLA---AAMCLHMQRTRRRRR-----PGEQVPPVPSPQ 228  
 DB 308 LLLVVAIVAGVLLMNMNSGLDPAWLSLSDGDLLEGNLPPEAPEQ 357

RESULT 15  
 ABL\_MOUSE STANDARD: PRT; 3726 AA.  
 ID ABL\_MOUSE  
 AC Q61329;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alpha-fetoprotein enhancer binding protein (AT motif-binding factor)  
 DE (AT-binding transcription factor 1).  
 GN ATRF1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BAIB/MK X ICR; TISSUE=Brain;  
 RX MEDLINE=96194902; PubMed=8654949;  
 RA Ido A., Miura Y., Watanabe M., Sakai M., Inoue Y., Miki T.,  
 Hashimoto T., Morinaga T., Nishi S., Tamaoki T.,

RT "Cloning of the cDNA encoding the mouse ATRF1 transcription factor."  
 RL Gene 168:227-231(1996).  
 CC -i- FUNCTION: Transcriptional activator that binds to the AT-rich core  
 CC sequence of the enhancer element of the AFP gene.  
 CC -i- SUBCELLULAR LOCATION: Nuclear.  
 CC -i- SIMILARITY: CONTAINS 4 HOMEBOX DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: D26046; BAA05046.1; -  
 DR HSSP: P20263; IOCp.  
 DR TRANSFAC; T03861; -  
 DR MGD; MGI:99948; Atrf1.  
 DR InterPro: IPR001356; Homeobox.  
 DR InterPro: IPR000822; znf\_C2H2.  
 DR InterPro: IPR003604; znf\_U1.  
 DR Pfam: PF00046; homeobox; 4.  
 DR Pfam: PF00096; zf-C2H2; 20.  
 DR ProDom: PD000010; Homeobox; 4.  
 DR SMART; SM00389; HOX; 4.  
 DR SMART; SM00355; znf\_C2H2; 22.  
 DR SMART; SM00451; znf\_U1; 7.  
 DR PROSITE; PS00027; HOMEBOX 1; 2.  
 DR PROSITE; PS00071; HOMEBOX 2; 4.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 15.  
 DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 9.  
 DR Transcription regulation; Activator; Zinc-finger; Metal-binding;  
 KW DNA-binding; Homeobox; Nuclear protein; Repeat.  
 FT ZN\_FING 79 103 C2H2-TYPE.  
 FT ZN\_FING 282 305 C2H2-TYPE.  
 FT ZN\_FING 641 664 C2H2-TYPE.  
 FT ZN\_FING 672 695 C2H2-TYPE.  
 FT ZN\_FING 727 751 C2H2-TYPE.  
 FT ZN\_FING 805 829 C2H2-TYPE (ATYPICAL).  
 FT ZN\_FING 946 969 C2H2-TYPE (DEGENERATE).  
 FT ZN\_FING 985 1009 C2H2-TYPE (ATYPICAL).  
 FT ZN\_FING 1041 1065 C2H2-TYPE (ATYPICAL).  
 FT ZN\_FING 1089 1113 C2H2-TYPE (ATYPICAL).  
 FT ZN\_FING 1233 1256 C2H2-TYPE.  
 FT ZN\_FING 1262 1285 C2H2-TYPE.  
 FT ZN\_FING 1370 1395 C2H2-TYPE.  
 FT ZN\_FING 1411 1433 C2H2-TYPE.  
 FT ZN\_FING 1439 1462 C2H2-TYPE.  
 FT ZN\_FING 1555 1579 C2H2-TYPE.  
 FT ZN\_FING 1606 1630 C2H2-TYPE.  
 FT ZN\_FING 1990 2013 C2H2-TYPE.  
 FT ZN\_FING 2152 2211 HOMEBOX 1.  
 FT ZN\_FING 2249 2308 HOMEBOX 2.  
 FT ZN\_FING 2335 2358 HOMEBOX 2.  
 FT ZN\_FING 2539 2561 C2H2-TYPE.  
 FT ZN\_FING 2650 2709 HOMEBOX 3.  
 FT ZN\_FING 2720 2743 C2H2-TYPE.  
 FT ZN\_FING 2952 3011 HOMEBOX 4.  
 FT ZN\_FING 3032 3056 C2H2-TYPE.  
 FT ZN\_FING 3552 3576 C2H2-TYPE.  
 FT ZN\_FING 461 491 POLY-GLU.  
 FT ZN\_FING 771 785 POLY-ALA.  
 FT ZN\_FING 1314 1317 POLY-ALA.  
 FT ZN\_FING 1734 1748 POLY-GLN.  
 FT ZN\_FING 1794 1799 POLY-GLN.  
 FT ZN\_FING 1856 1863 POLY-GLN.  
 FT ZN\_FING 2044 2059 POLY-PRO.  
 FT ZN\_FING 2405 2408 POLY-ALA.  
 FT ZN\_FING 3216 3220 POLY-PRO.  
 FT ZN\_FING 3380 3409 POLY-GLN.  
 FT ZN\_FING 3412 3420 POLY-GLN.  
 FT ZN\_FING 3534 3550 POLY-GLY.





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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:25:46 ; Search time 19 Seconds  
(Without alignments)  
1189.031 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242  
Sequence: 1 MVLAPAWSPPTVLLLLLL.....RPEQVPPVPSDOLLVEH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	2 I38440	flt3 ligand - huma
2	864.5	69.6	245	2 S43293	FLT3/FLK2 ligand (
3	834	67.1	178	2 I39076	flt3 ligand alterm
4	768.5	61.9	231	2 A49265	flt3/Flk2 ligand
5	606.5	48.8	220	2 S43291	FLT3/FLK2 ligand (
6	606.5	48.8	220	2 I58343	flt3 ligand isoform
7	93	7.5	1217	2 T22672	hypothetical prote
8	92	7.4	661	1 TNBE12	74k alpha trans-in
9	89.5	7.2	474	1 T19543	hypothetical prote
10	89	7.2	387	1 I48201	adhalin - golden h
11	89	7.2	793	1 S60735	splicing factor SF
12	88.5	7.1	238	2 AB1990	hypothetical prote
13	88.5	7.1	1386	2 T00257	hypothetical prote
14	88	7.1	753	2 J00532	OP protein - Kenne
15	87.5	7.0	479	1 A33290	protein-tyrosine-p
16	87	7.0	910	2 A53337	tyrosine kinase re
17	86.5	7.0	590	2 A40437	glutamic acid-rich
18	86	6.9	299	2 T17832	hypothetical prote
19	86	6.9	485	2 A33647	sulfated surface g
20	86	6.9	746	2 T28004	hypothetical prote
21	85	6.8	289	2 A87646	hypothetical prote
22	85	6.8	366	2 A37374	FC gamma (Igg) rec
23	84	6.8	263	2 T03162	gamma-globulin 6
24	84	6.8	757	2 A39283	gamma-globulin 1 car
25	83.5	6.7	199	2 E75630	hypothetical prote
26	83.5	6.7	530	2 A45690	transactivator EBN
27	83	6.7	1509	2 T19486	hypothetical prote
28	82.5	6.6	418	2 T19800	hypothetical prote
29	82.5	6.6	426	2 I36948	Ig epsilon-chain -

30	82.5	6.6	512	2 D40829	activin receptor 1
31	82.5	6.6	513	2 J01484	activin receptor p
32	82	6.6	106	2 T06479	proline/leucine-r1
33	82	6.6	834	2 T23837	hypothetical prote
34	81.5	6.6	485	2 C75460	hypothetical prote
35	81.5	6.6	488	2 S13423	stromelysin 3 (EC
36	81.5	6.6	958	2 T13593	hypothetical prote
37	81.5	6.6	1119	2 T50995	related to cytoke
38	81	6.5	196	2 B48232	cysteine-rich exte
39	81	6.5	209	2 A48232	cysteine-rich exte
40	81	6.5	294	2 A12016	hypothetical prote
41	81	6.5	388	2 S15591	probable transpos
42	81	6.5	428	1 EHHU	Ig epsilon chain C
43	80.5	6.5	636	2 JMO047	class I cyto kinase
44	80.5	6.5	1176	2 T49482	hypothetical prote
45	80.5	6.5	1306	2 T13592	hypothetical prote

## ALIGNMENTS

RESULT 1  
I38440  
flt3 ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence.revision 29-May-1998 #text\_change 01-Dec-2000  
C:Accession: I38440; I39075; S43292  
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe  
Blood 83, 2795-2801, 1994  
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo  
A:Reference number: I38440; MUID:94235842; PMID:8180375  
A:Accession: I38440  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-235 <RES>  
A:Cross-references: EMBL:U02874; NID:9494978; PIDN:AA19825.1; PID:9494979  
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.  
Oncogene 11, 1165-1172, 1995  
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.  
A:Reference number: I39075; MUID:96032581; PMID:7566977  
A:Accession: I39075  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-235 <RES>  
A:Cross-references: EMBL:U02874; NID:91072036; PIDN:AA90949.1; PID:91072037  
R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;  
felt, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik  
Nature 368, 643-648, 1994  
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic  
A:Reference number: S43290; MUID:94195428; PMID:8145851  
A:Accession: S43292  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-71, 'A', 73-235 <HAN>  
A:Cross-references: GB:U04806; NID:9483844; PIDN:AA1999.1; PID:9483845  
A:Note: the authors translated the codon AGR for residue 25 as Met  
C:Genetics:  
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3  
Query Match 100.0%; Score 1242; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5, 4e-99;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MVLAPAWSPPTVLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSVDLLDDYPTV 60  
DB 1 MVLAPAWSPPTVLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSVDLLDDYPTV 60  
OY 61 ASNLODELGGLMRLVLAORMERLKTIVAGSKMGLERVNTETHPVTKCAFOPPSCL 120  
DB 61 ASNLODELGGLMRLVLAORMERLKTIVAGSKMGLERVNTETHPVTKCAFOPPSCL 120  
OY 121 RVQNTISRLQENSEQLVALKPWITRONFSRCLELQCOQPSSTLPPWSPRPLEATAPT 180  
DB 121 RVQNTISRLQENSEQLVALKPWITRONFSRCLELQCOQPSSTLPPWSPRPLEATAPT 180

Db 121 REVQTNISRLQETSEQLVAKFWITRONFSRCLLELOCPDSSSTLPPPSPPLEATAPT 160

QY 181 APQPLLILLLPVGLLLAAAMCLHMORTRRRTPRGEQVPPVPSFODLLVEH 235

Db 181 APQPLLILLLPVGLLLAAAMCLHMORTRRRTPRGEQVPPVPSFODLLVEH 235

## RESULT 2

SA43293  
 FLT3/Flk2 ligand (clone S109) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
 C:Accession: S43293  
 R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kelf, A.; Muench, M.; Kelnher, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.  
 Nature 368, 643-648, 1994  
 A:Title: Ligand for FLT3/Flk2 receptor tyrosine kinase regulates growth of haematopoietic  
 A:Reference number: S43290; MUID:94195428; PMID:8145851  
 A:Accession: S43293  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-245 <HAN>  
 A:Note: the authors translated the codon AGT for residue 25 as Met

Query Match 69.6%; Score 864.5; DB 2; Length 245;  
 Best Local Similarity 73.0%; Pred. No. 1.2e-66;  
 Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

QY 1 MYVLAPWSPFTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

Db 1 MYVLAPWSPFTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

QY 61 ASNLQDEELCGLMRLVLAQRMERLKTVAAGSKMOGLLEEVNTEIHFTVKCAFOPPSCL 120

Db 61 ASNLQDEELCGALMRLVLAQRMERLKTVAAGSKMOGLLEEVNTEIHFTVKCAFOPPSCL 120

QY 121 RFVQTNISRLQETSEQLVAKFWITRONFSRCLLELOCPDSSSTLPPPSPPLEATAPT 180

Db 121 RFVQTNISRLQETSEQLVAKFWITRONFSRCLLELOCPDSSSTLPPPSPPLEATAPT 177

QY 181 APQPLLILLLPVGLLLAAAMCLHMORTRRRTPRGEQVPPVPS 227

Db 178 WPRPHRGEDTEAHRGESP-----ARGLTAMTQKRLARGRLPMAPLPSP 222

QY 228 Q 228

Db 223 E 223

## RESULT 3

139076  
 Flt3 ligand alternatively spliced isoform - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
 C:Accession: I39076  
 R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.  
 Oncogene 11, 1165-1172, 1995  
 A:Title: Structural analysis of human and murine flt3 ligand genomic loci.  
 A:Reference number: I39075; MUID:96032581; PMID:7566977  
 A:Accession: I39076  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-178 <RES>  
 A:Cross-References: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038  
 C:Genetics:  
 A:introns: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match 67.1%; Score 834; DB 2; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-64;  
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVLAPWSPFTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

Db 1 MYVLAPWSPFTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

Db 1 MYVLAPWSPFTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

QY 61 ASNLQDEELCGLMRLVLAQRMERLKTVAAGSKMOGLLEEVNTEIHFTVKCAFOPPSCL 120

Db 61 ASNLQDEELCGLMRLVLAQRMERLKTVAAGSKMOGLLEEVNTEIHFTVKCAFOPPSCL 120

QY 121 RFVQTNISRLQETSEQLVAKFWITRONFSRCLLELOCP 160

Db 121 RFVQTNISRLQETSEQLVAKFWITRONFSRCLLELOCP 160

## RESULT 4

A49265  
 FLT3/Flk-2 ligand precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 08-Oct-1999  
 C:Accession: A49265; I49347; I49346; S43290  
 R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl  
 D.; Williams, D.E.; Beckmann, M.P.  
 Cell 75, 1157-1167, 1993

A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a  
 A:Reference number: A49265; MUID:94084791; PMID:7505204  
 A:Accession: A49265  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-231 <LYM>  
 A:Cross-References: EMBL:L23636; NID:g439441; PIDN:AAA39436.1; PID:g439442  
 R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.  
 Oncogene 11, 1165-1172, 1995  
 A:Title: Structural analysis of human and murine flt3 ligand genomic loci.  
 A:Reference number: I39075; MUID:96032581; PMID:7566977  
 A:Accession: I49347  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-163, 'G', '165, 'HYAG' <RES>  
 A:Cross-References: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041  
 A:Accession: I49346  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-197, 'L', '198-231 <RES>  
 A:Cross-References: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040  
 R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;  
 felt, A.; Muench, M.; Kelnher, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik  
 Nature 368, 643-648, 1994  
 A:Title: Ligand for FLT3/Flk2 receptor tyrosine kinase regulates growth of haematopoi  
 A:Reference number: S43290; MUID:94195428; PMID:8145851  
 A:Accession: S43290  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-197, 'L', '198-231 <HAN>

A:Experimental source: Clone T110  
 A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-  
 C:Genetics:  
 A:introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3  
 C:Keywords: transmembrane protein

Query Match 61.9%; Score 766.5; DB 2; Length 231;  
 Best Local Similarity 70.3%; Pred. No. 1.8e-58;  
 Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MYVLAPWSPFTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRELSYLLQDYPVTV 59

Db 1 MYVLAPWSPFTYLLLLLSGLSGTODCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

QY 60 VASNLQDEELCGLMRLVLAQRMERLKTVAAGSKMOGLLEEVNTEIHFTVKCAFOPPSCL 119

Db 61 VASNLQDEELCGLMRLVLAQRMERLKTVAAGSKMOGLLEEVNTEIHFTVKCAFOPPSCL 120

QY 120 LRFVQTNISRLQETSEQLVAKFWITR--QNFSCRLELOCPDSSSTLPPPSPPLEAT 177

Db 121 LRFVQTNISRLQETSEQLVAKFWITR--QNFSCRLELOCPDSSSTLPPPSPPLEAT 180

QY 178 APVAPQPP--LLLLLLPVGLLLAAAMCLHMORTRRRTPRGEQVPPVPS 227

Db 181 ELPEPRRROLLLLLLLPLFLVLLAAMGLRMQARRR-----GELHGVLP 228

## RESULT 5

S43291  
FLR3/FLK2 ligand (clone T118) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
C:Accession: S43291  
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kretz, A.; Muench, M.; Kellner, G.; Nankawa, R.; Kennick, D.; Roncarolo, M.G.; Zlotnik, A.  
A:Title: Ligand for FLR3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells.  
A:Reference number: S43290; MUID:94195428; PMID:8145851  
A:Accession: S43291  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-220 <HANN>

## Query Match

Best Local Similarity 48.8%; Score 606.5; DB 2; Length 220;  
Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

Qy 1 MTVLAPAMSP-TTYLLLLLSGLSGTQDCSFQHSPISSDPAVKIRELSIDYLLQDYPVT 59  
Db 1 MTVLAPAMSPSSLLLLLLLSPCLRGTPDCYFSHSPISSNFVKFRLTDHLKDYVT 60  
Qy 60 VASNLQDEELCGLMRLVLAQRMERLKYAGSKMGLLEVNTEIHFTVTCARPPSC 119  
Db 61 VAVNLQDEKCKALMSFLAQRWIEQLKYAGSKMGLLEVNTEIHFTVTCARPPSC 120  
Qy 120 LRFVQTNISRLQETSQDLVALKPMITR--ONFSRCLELOCOPDSSTLPWPMSRP---- 173  
Db 121 LRFVQTNISHLKQTCQQLALAKPCICKACONFSRCLEVOCPQNG-----GPAQHNG 174  
Qy 174 ---LEATAPAPAPPLLL-----LLLPVGLLLAA 201  
Db 175 ATRLATATLTLVCPGLLLPLVGTSHMFFLPFLSLSS 212

## RESULT 6

I58343  
flt3 ligand isoform 5H - mouse  
C:Species: Mus sp. (mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I58343  
R:Ljman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, K.  
Oncogene 10, 149-157, 1995  
A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand.  
A:Reference number: I58343; MUID:95124710; PMID:7824267  
A:Accession: I58343  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-220 <RES>  
A:Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1; PID:g913480

## Query Match

Best Local Similarity 48.8%; Score 606.5; DB 2; Length 220;  
Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

Qy 1 MTVLAPAMSP-TTYLLLLLSGLSGTQDCSFQHSPISSDPAVKIRELSIDYLLQDYPVT 59  
Db 1 MTVLAPAMSPSSLLLLLLLSPCLRGTPDCYFSHSPISSNFVKFRLTDHLKDYVT 60  
Qy 60 VASNLQDEELCGLMRLVLAQRMERLKYAGSKMGLLEVNTEIHFTVTCARPPSC 119  
Db 61 VAVNLQDEKCKALMSFLAQRWIEQLKYAGSKMGLLEVNTEIHFTVTCARPPSC 120  
Qy 120 LRFVQTNISRLQETSQDLVALKPMITR--ONFSRCLELOCOPDSSTLPWPMSRP---- 173  
Db 121 LRFVQTNISHLKQTCQQLALAKPCICKACONFSRCLEVOCPQNG-----GPAQHNG 174

Qy 174 ---LEATAPAPAPPLLL-----LLLPVGLLLAA 201  
Db 175 ATRLATATLTLVCPGLLLPLVGTSHMFFLPFLSLSS 212

## RESULT 7

T22672  
hypothetical protein F54F12.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T22672  
R:Barlow, K.  
Submitted to the EMBL Data Library, November 1996  
A:Reference number: T22672  
A:Accession: T22672  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1217 <MIL>  
A:Cross-references: EMBL:T22672; NID:e1062020; PIDN:CAB04464.1; GSPDB:GN00021; CESP:F54F12  
A:Experimental source: Clone F54F12  
C:Genetics:  
A:Gene: CESP:F54F12.1  
A:Map position: 3  
A:Insertions: 742/2; 826/1; 922/3; 972/1; 1024/2; 1102/1

## Query Match

Best Local Similarity 7.5%; Score 93; DB 2; Length 1217;  
Matches 38; Conservative 33; Mismatches 68; Indels 22; Gaps 6;

Qy 83 MERLKYAGSKMGL---LEVNTEIHFTVTCARPPSCLERFVQTNISRLQETSQDLV 139  
Db 627 MDAAKAVDGTYSYIDALEKLSMDLDFOKYKFEATATKAMD---FFASYASMLA 682  
Qy 140 ALKPWITRQNSRCLQEQDSSSTL---PPWSPRLPAPAPAP-----OPPLLLLL 191  
Db 683 ALRPOPTSDPTAAAPVIRPNKSGSLNGNSPSPPLLPVASSPTAATPESNMLLYIT 742  
Qy 192 LRVGLLLAA-----AMCLHWQRTARRTPRGEQVPVPS 227  
Db 743 GAVGGLLVALLIGVILFFVFOKKKKKEDKPD--PPAPLP 781

## RESULT 8

TNBE12  
74K alpha trans-inducing protein - human herpesvirus 3  
C:Species: human herpesvirus 3, varicella-zoster virus  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 16-Jul-1999  
C:Accession: C27342  
R:Davidson, A.D.; Scott, J.E.  
J. Gen. Virol. 67, 1759-1816, 1986  
A:Title: The complete DNA sequence of varicella-zoster virus.  
A:Reference number: A27345; MUID:86306657; PMID:3018124  
A:Accession: C27342  
A:Molecule type: DNA  
A:Residues: 1-661 <DAV>  
A:Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27895.1; PID:g60001  
C:Genetics:  
A:Gene: 12  
C:Superfamily: herpesvirus 77K alpha trans-inducing protein  
C:Keywords: trans-inducing protein; transcription regulation

## Query Match

Best Local Similarity 7.4%; Score 92; DB 1; Length 661;  
Matches 61; Conservative 29; Mismatches 103; Indels 36; Gaps 11;

Qy 19 LLSGLSGTQDCS---FQHSPISSDPAVKI--RELSIDYLLQDYPVTVASNLQDEELCG 71  
Db 79 LSPVLAQSTERHSVLLGLAHNNVPESLVSCMSNDVHDGFMQRYMETIQRCLDLKLSGD 138  
Qy 72 GLMRLVLAQRMERLKYAGSKMGLLEVN---TEIHFTVTCARPPSCLERFV 123  
Db 139 GLM-WVYENTYQWYLKYTTGAEPVTSKVNKKSKSTVLLFSSVAVANPISRHPKSKVI 197

OY 124 QTNISRLQETSEQLVAKPWITRONFSRCLELOCOPDSSLTPPWSP-RPLEATAPAP 182  
 Db 198 NSBYRGICQELRRLALGAVQYKYM--YFMR-----PDDEPTNPSPPDRIRHVOEIAATAT 247  
 OY 183 QPPLLILLLLLPVGLILLAAAMCLHMORTRRTPRPGQVPPVPSPODL 231  
 Db 248 GYGMWMLFLLVD-----ARVCRHLKLOFRIRKGRASV---IPDDL 287

## RESULT 9

T19543

hypothetical protein C28D4.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T19543

R:McMurray, A.  
submitted to the EMBL Data Library, November 1996

A:Reference number: Z19139

A:Accession: T19543

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-474 &lt;MIL&gt;

A:Cross-references: EMBL:Z82259; PDB:CA05129.1; GSPDB:GN00022; CESP:C28D4.2

A:Experimental source: clone C28D4

C:Genetics:

A:Gene: CESP:C28D4.2

A:Map position: 4

A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

## Query Match

7.2%; Score 89.5; DB 2; Length 474;

Best local similarity 24.1%; Pred. No. 5.5;

Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

OY 27 TDQC-----SFQHS-PISSDFAVKIREL-SDYLQDYPVYASNLQDELCGLMRL 76  
 Db 65 TDCVDLKVFSKFDSSAPISGELFRAFLCAKYL-----GCAMRK 106  
 OY 77 VLAQRMERKITYAGSMQGLLERNTEHFVVKCAQPPSCLR-FVQTNISRLQET- 134  
 Db 107 VKLEEF-RIRATIG-MSNLFLVELPAH-LPIQMEPKALLRVQCSDIDLLSESV 162  
 OY 135 -----SEDLVAKPWITRONFSRCLELOC-----OPDSSLTPPWSPR-PLBATA 178  
 Db 163 VFTLLSRNIGPKMLGVPGRGREFQIPSRALOCLEISKGLSLPIYARVHTLDAP 222  
 OY 179 PTAPQPLLILLLLPVGLILLAAAMCLHMORTRRTP--RPG-----QVPPVPSPOD 229  
 Db 223 PKBPQ-----TLQTAQWLERF---KKPAGRIEMVLTQAKVPSDYEST 266  
 OY 230 LLVE 234  
 Db 267 ITVAQ 271

## RESULT 10

I48201

adhalin - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Jun-2000

C:Accession: I48201

R:Roberts, S.L.; Campbell, K.P.  
FEBS Lett. 364, 245-249, 1995

A:Title: Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.

A:Reference number: I48201; MID:95278335; PMID:7758576

A:Accession: I48201

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-387 &lt;RES&gt;

A:Cross-references: EMBL:U21677; NID:q726481; PDB:AAA81645.1; PID:q726482

C:Superfamily: mouse adhalin

## Query Match

7.2%; Score 89; DB 2; Length 387;

Best local similarity 23.4%; Pred. No. 4.8;

Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

OY 11 TTVLLLLLSLSCGTQDCSFQHSPISSDFAVKIRELDYLDYVPVYASNLQDELC 70  
 Db 115 TTRQRLILLI-----EDEGRRLPYQAEFLVRSHVEVL-----PSTRANFL--TAL 161  
 OY 71 GGLMRL-----VLAQRMERKITYAGSMQGLLERNTEHFVVK- 110  
 Db 162 GGLMELGELQLNLITNSALDRGVRPLPIEGRKEGVYIKVGSATPFSCLTKVASPSYAR 221  
 OY 111 CAFQPP--SC-----LRFVQTNISRLQETSEQLVAKPWITRONFSRCLELOCQPD 161  
 Db 222 CAQGQPPLLSCYSLAPHFVDMCNVSLVDKSVPEPLD-----EVPFGD 266  
 OY 162 SSTLPWPSPRPLEAT-----APTAPQPLLILLLLPVGLILLAAAMC----- 204  
 Db 267 GLEHDPFCPPPEATGRDLALALVTLVPLVALLL--TLLVIMCCRREGQLKR 323  
 OY 205 -----LHMORTRRTPRP-----GEQVPP-VSPQ-DLL 231  
 Db 324 MATSDIQMVHCHTGHNTTEELROMAARREVPRPLSTLPMENVRGRLPRVDSAQVPL 383  
 OY 232 LVEH 235  
 Db 384 LDQH 387

## RESULT 11

S60735

splicing factor SF3a 120K chain - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000

C:Accession: S60735; S60733

R:Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Bilbe, G.  
RNA 1, 260-272, 1995

A:Title: Mammalian splicing factor SF3a120 represents a new member of the SUPR family

A:Reference number: S60733; MID:96079958; PMID:7489498

A:Accession: S60735

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-793 &lt;KRA&gt;

A:Cross-references: EMBL:X85237; NID:g899297; PDB:CAA5494.1; PID:g899298

A:Accession: S60733

A:Molecule type: protein

A:Residues: 51-62; 82-94; 270-275; 397-414; 448-463 &lt;KRA&gt;

A:Gene: GDB:SF3A120; PRP21; SAP114

A:Cross-references: GDB:9955873

A:Map position: 22q12.1-22qter

C:Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology

C:Keywords: pre-mRNA splicing

E:714-790/Domain: ubiquitin homology &lt;UBH&gt;

Query Match 7.2%; Score 89; DB 1; Length 793;

Best local similarity 22.3%; Pred. No. 11;

Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

OY 4 LAPAWSPTTYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELDYLDYPVYASN 63  
 Db 401 LPPAPAPDFEYL-----SPITGE--KI-----PASK 424  
 OY 64 LQDEELGGIMRLVLAQRWME-FLKTV-----AGSMQGLLERNTEHFV 107  
 Db 425 MQEHRIG-----LDRPRLQDRSTIREKQSDDEVYAPGLDISSIKOLAER-RDIFG 478  
 OY 108 VTRCA-----FQPPSCLEF-----VQTNISRLQETSEQLVAKPWIT 145  
 Db 479 VERTALGKKTGEIEIKPEKRYWHDGSSGSMARTQAQAQANIT--LOFQEAIRHKKGLV 536  
 OY 146 -----TRQNF--SRCLELOC-----DSSTLP-----PPWSPRPLEAT---APT 180  
 Db 537 PEDDTKEIKIPSKPNEIPQPPPPSSATNIPSSAPITSVPRPMPVPVKTIVSAVAV 596



OY 181 APOPELLELLLPVGLLLAAWCLHMQR-----RRTPREGQVPP---VSP 227  
 Db 597 MPRPMASVYRLPPGSIYIAMPPIIINAVVPMPSAPPIMAPRRPPIVPAFVAP 656

## RESULT 12

AB1990  
 hypothetical protein al11471 [Imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AB1990

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium An

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AB1990

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-238 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA077837.1; PID:g17135292; GSPDB:GN00179

A:Experimental source: strain PCC 7120

A:Genetics:

A:Gene: al11471

Query Match 7.1%; Score 88.5; DB 2; Length 238;

Best Local Similarity 20.8%; Pred. No. 3;

Matches 44; Conservative 32; Mismatches 59; Indels 77; Gaps 9;

OY 34 HSPISDFAVKIRELSDYLLQDY--PVTASNLQDELQGLMRLVLAQRMERLQTV 90

Db 84 HSKKTTTYESINEVCNOYLKSYKKPLVLI-----QILG-W-----SGLRMKYKTV 131

OY 91 GSKMGLLEVNTEHIFVTKCAFQPPSCLEFYQFNISRLQ-----EISEQ 137

Db 132 DDDDTDISPEISTEV-----VVRKIPKVIETPKIVKPKQTKEDIKTLES 174

OY 138 LVALKPWITRONFSRCLQCOPODSSITLPPPM---SPRPLEATAPAPOPPLLLLPV 194

Db 175 PGLKRP--TKPIPKLIEPKKSDSKNLQRPIDSPKPIKNSQPEAKRYV----- 223

OY 195 GLLLLAAWCLHMQRTRRRTPREGQVPPVPS 226

Db 224 -----EPPKPMERYPKKPS 237

## RESULT 13

T00257  
 hypothetical protein KIAA0476 - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 21-Jul-2000

C:Accession: T00257

R:Seiki, N.; Ohita, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.

DNA Res. 4, 345-349, 1997

A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human

A:Reference number: 214085; MUID:98116662; PMID:9455484

A:Accession: T00257

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1386 <SEK>

A:Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BA32321.1; PID:g3413914

A:Experimental source: brain

A:Genetics:

A:Note: KIAA0476

Query Match 7.1%; Score 88.5; DB 2; Length 1386;

Best Local Similarity 23.1%; Pred. No. 23;

Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

OY 21 SSGLSGQDPSFQHSPISSFAVKIRELSYLLQDYVTVASNLQDELQ-----GGLMRL 76

Db 1104 SAGASGSKDAPVPGP-----GPVLSDRRLCLA--LDEPOLCNGHMGASRR 1148

OY 77 VLAORMERLKTAVGSKMGLLEVNTEHIFVTKCAFQPPSCLEFYQFNISRLQENSE 136

Db 1149 VESGAMAYLSPLVLRKELSEVENEGSEV-----LALPELSANPIITWNLMTFQRL-- 1201

OY 137 QLVALKPWITRONFSRCLQCO--PDSSITLPPM--SPRPLEA-----TAPTAPOP 185

Db 1202 RLPSILPLGLVLAS-----CDGFSHQASAPMLTTPDPASVQVRLMDVLTTPPNNSCPP 1253

OY 186 LLLLLLPVGLLLAAWCLHMQRTRRRTPREGQVPPVPSQDOLLVE 234

Db 1254 LLYL-----WRVHSQ--IPQRVWVG---VPASLSLALLE 1284

## RESULT 14

J00532

OP protein - Kennedy yellow mosaic virus

C:Species: Kennedy yellow mosaic virus

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 28-May-1999

C:Accession: J00532

R:Ding, S.; Keese, P.; Gibbs, A.

J. Gen. Virol. 71, 925-931, 1990

A:Title: The nucleotide sequence of the genomic RNA of Kennedy yellow mosaic tymovir

A:Reference number: J00532; MUID:90218040; PMID:2324710

A:Accession: J00532

A:Molecule type: mRNA

A:Residues: 1-753 <DIN>

A:Cross-references: GB:000637; NID:g221969; PIDN:BA00531.1; PID:d100986; PID:g22197

A:Experimental source: strain Jervais Bay isolate

Query Match 7.1%; Score 88; DB 2; Length 753;

Best Local Similarity 22.3%; Pred. No. 12;

Matches 41; Conservative 19; Mismatches 58; Indels 66; Gaps 7;

OY 100 RVNTEHIFVTKCAFQPPSCLEF---VQTNIS-----RLQETSEQLVALKPMTR 147

Db 420 RLSTQPPSSPQSTSSPPSPPTDASGIQPLASPPSKRKESLPHPSHQ---PPSHK 475

OY 148 QNFSR---CLELCOPODSSITLPPMSPRPLEATAPAPOPPLLLLP----- 193

Db 476 RNLRRHSALPLLIPIHPTKTQPPHVPQP--TAGPTPHPPPTKPIPLHPKSDQERHSP 533

OY 194 -----VGLLLAAWCLHMQRTRRRTPREGQVPPVPS 226

Db 534 PPVDFHDCQPSPTSHVGVYRRLGSGISLPFKLAFW-----RRSPNPARHLPPPP 586

OY 227 PDL 230

Db 587 PKRL 590

## RESULT 15

A32290

protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly (Drosophi

C:Species: Drosophila melanogaster

C>Date: 05-Oct-1989 #sequence\_revision 25-Apr-1997 #text\_change 11-Jun-1999

C:Accession: A32290

R:Edgar, B.A.; O'Farrell, P.H.

Cell 57, 177-187, 1989

A:Title: Genetic control of cell division patterns in the Drosophila embryo.

A:Reference number: A32290; MUID:89195217; PMID:2702688

A:Accession: A32290

A:Molecule type: mRNA

A:Residues: 1-479 <EDG>

A:Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; PID:g158508

R:Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.

EMBO J. 9, 3565-3571, 1990

A:Title: Complementation of fission yeast cdc2(1s) and cdc25(1s) mutants identifies t

A:Reference number: S12008; MUID:91006056; PMID:2120044

A:Accession: S12008

A:Molecule type: mRNA

A:Residues: 1-227, 'A', 229-479 <JIM>

A:Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1; PID:g7707

